

2 32  
CTT TCA GAA GCC CGG GAG AGC GTC TTG GGG GAT TTG CTG AAG GTT GTG CTG TAC AGC CTG  
leu ser glu ala arg glu ser val leu gly asp leu leu lys val val leu tyr ser leu

62 92  
GGC AGT GCC CAG AGT GCC CTC TTC TTG CAG CAT GGC CTG GCC ACC CAG AGG GCC CTT GTG  
gly ser ala gln ser ala leu phe leu gln his gly leu ala thr gln arg ala leu val

122 152  
TCC AAG TTC CCG GAG CTG CTG TTC GAG GAG GAC ACG GAG CTG TGT GCC GAC CTG TGC CTG  
ser lys phe pro glu leu leu phe glu glu asp thr glu leu cys ala asp leu cys leu

182 212  
AGG CTC CTA CGA CAC TGT GGC AGC CGC ATC AGC ACC ATC CGC ACG CAC GCC AGC GCC TCG  
arg leu leu arg his cys gly ser arg ile ser thr ile arg thr his ala ser ala ser

242 272  
CTG TAC CTG CTC ATG CGA CAG AAC TTC GAG ATC GGC CAC AAC TTT GCC CGT GTG AAG ATG  
leu tyr leu leu met arg gln asn phe glu ile gly his asn phe ala arg val lys met

302 332  
CAG GTC ACC ATG TCT CTC TCG TCC CTG GTG GGG ACG ACG CAG AAC TTC AGT GAA GAG CAC  
gln val thr met ser leu ser ser leu val gly thr thr gln asn phe ser glu glu his

362 392  
CTG CGA CGT TCA CTC AAA ACC ATC CTC ACC TAT GCT GAG GAG GAC ATG GGG CTG CGG GAC  
leu arg arg ser leu lys thr ile leu thr tyr ala glu glu asp met gly leu arg asp

422 452  
AGC ACC TTC GCA GAG CAG GTC CAG GAC CTG ATG TTC AAC CTG CAC ATG ATC CTG ACG GAC  
ser thr phe ala glu gln val gln asp leu met phe asn leu his met ile leu thr asp

482 512  
ACG GTG AAG ATG AAG GAA CAC CAG GAG GAC CCT GAG ATG CTC ATC GAC CTC ATG TAC AGA  
thr val lys met lys glu his gln glu asp pro glu met leu ile asp leu met tyr arg

542 572  
ATT GCC CGG GGC TAC CAG GGC TCA CCG GAC CTT CGG CTG ACC TGG TTG CAG AAC ATG GCC  
ile ala arg gly tyr gln gly ser pro asp leu arg leu thr trp leu gln asn met ala

602 |xxxxxxxxxxxxxxxx transmembrane domain xxxxxxxxxxxx  
GGG AAG CAC GCG GAG CTG GGC AAC CAC GCC GAG GCC GCC CAG TGC ATG GTG CAC GCG GCC  
gly lys his ala glu leu gly asn his ala glu ala ala gln cys met val his ala ala

xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx| 692  
GCC CTC GTG GCT GAG TAC CTC GCC CTG CTC GAG GAC CAC CGC CAC CTG CCC GTG GGC TGC  
ala leu val ala glu tyr leu ala leu leu glu asp his arg his leu pro val gly cys

722 752  
GTT TCC TTC CAG AAC ATC TCA TCC AAT GTG CTA GAG GAG TCC GCC ATC TCC GAC GAC ATC  
val ser phe gln asn ile ser ser asn val leu glu glu ser ala ile ser asp asp ile

782 812  
CTG TCG CCC GAC GAG GAG GGC TTC TGC TCC GGG AAG CAC TTC ACT GAG CTG GGG CTG GTA  
leu ser pro asp glu glu gly phe cys ser gly lys his phe thr glu leu gly leu val

842 872  
GGG TTG CTG GAA CAG GCA GCC GGC TAC TTC ACC ATG GGC GGG CTC TAC GAG GCG GTG AAT  
gly leu leu glu gln ala ala gly tyr phe thr met gly gly leu tyr glu ala val asn

FIG. 1 (1 of 3)

```

902                               932
GAG GTC TAC AAG AAC CTC ATC CCC ATC CTG GAA GCC CAC CGT GAC TAC AAG AAG CTG GCC
glu val tyr lys asn leu ile pro ile leu glu ala his arg asp tyr lys lys leu ala

962                               992
GCG GTG CAC GGC AAA CTG CAG GAG GCC TTC ACC AAG ATC ATG CAC CAG AGT TCC GGC TGG
ala val his gly lys leu gln glu ala phe thr lys ile met his gln ser ser gly trp

1022                               |xxxxx ITAM xxxx|1052
GAG CGC GTG TTC GGG ACG TAT TTC CGC GTG GGC TTC TAC GGC GCC CAC TTC GGT GAC CTG
glu arg val phe gly thr tyr phe arg val gly phe tyr gly ala his phe gly asp leu

1082                               1112
GAT GAG CAG GAG TTT GTG TAC AAG GAG CCA TCG ATC ACG AAG CTG GCA GAG ATC TCA CAC
asp glu gln glu phe val tyr lys glu pro ser ile thr lys leu ala glu ile ser his

1142                               1172
CGG CTG GAG GAG TTC TAC ACG GAG AGA TTT GGC GAC GAC GTC GTT GAG ATT ATC AAA GAC
arg leu glu glu phe tyr thr glu arg phe gly asp asp val val glu ile ile lys asp

1202                               1232
TCT TAC CCT GTG GAC AAG TCC AAG CTT GAC TCA CAA AAG GCC TAC ATC CAG ATC ACG TAT
ser tyr pro val asp lys ser lys leu asp ser gln lys ala tyr ile gln ile thr tyr

1262                               1292
GTG GAA CCG TAC TTT GAT ACC TAC GAG CTC AAG GAC CGG GTG ACC TAC TTT GAC CGC AAC
val glu pro tyr phe asp thr tyr glu leu lys asp arg val thr tyr phe asp arg asn

1322                               1352
TAT GGG CTT CGC ACA TTC CTG TTC TGC ACG CCG TTC ACG CCG GAT GGG CGC GCA CAC GGG
tyr gly leu arg thr phe leu phe cys thr pro phe thr pro asp gly arg ala his gly

1382                               1412
GAG CTG CCC GAG CAA CAC AAG CGT AAG ACG CTG CTC AGC ACC GAC CAC GCC TTC CCC TAC
glu leu pro glu gln his lys arg lys thr leu leu ser thr asp his ala phe pro tyr

1442                               1472                               |xxxxxxxxxxxx
ATC AAG ACT CGC ATC CGT GTG TGC CAC CGG GAG GAG ACG GTG CTG ACG CCA GTG GAG GTG
ile lys thr arg ile arg val cys his arg glu glu thr val leu thr pro val glu val

xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx Coiled coil 1 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
GCC ATC GAG GAC ATG CAG AAG AAG ACA CGG GAG CTG GCC TTT GCC ACC GAG CAG GAC CCA
ala ile glu asp met gln lys lys thr arg glu leu ala phe ala thr glu gln asp pro

xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx|
CCA GAT GCT AAG ATG CTA CAG ATG GTG CTT CAG GGC TCT GTA GGG CCC ACC GTG AAC CAG
pro asp ala lys met leu gln met val leu gln gly ser val gly pro thr val asn gln

1622                               1652
GGT CCC CTG GAG GTG GCC CAG GTG TTT TTA GCA GAG ATC CCG GAA GAC CCC AAG CTC TTC
gly pro leu glu val ala gln val phe leu ala glu ile pro glu asp pro lys leu phe

1682                               1712
CGG CAT CAC AAC AAA TTG CGG CTC TGC TTC AAG GAC TTC TGC AAG AAA TGT GAG GAT GCG
arg his his asn lys leu arg leu cys phe lys asp phe cys lys lys cys glu asp ala

|xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx Coiled coil 2 xxxxxxxxxxxxxxxxxxxxxxxxxxx
CTG CGG AAA AAT AAG GCC CTG ATT GGG CCG GAC CAG AAG GAG TAC CAC CGT GAG CTG GAG
leu arg lys asn lys ala leu ile gly pro asp gln lys glu tyr his arg glu leu glu

```

FIG. 1 (2 of 3)

09736968-161201

```

XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX!
CGC AAC TAC TGC CGC CTG CGG GAG GCT CTG CAG CCC CTG CTT ACC CAG CGC CTG CCC CAG
arg asn tyr cys arg leu arg glu ala leu gln pro leu leu thr gln arg leu pro gln

1862                                     1892
CTG ATG GCA CCC ACC CCA CCC GGC CTC AGG AAC TCC TTG AAC AGA GCA AGT TTC CGA AAG
leu met ala pro thr pro pro gly leu arg asn ser leu asn arg ala ser phe arg lys

1922                                     1952
GCA GAC CTC TGA GCC CAC AAG GAC CAA AGC TGT ACC TAG AGG AAC CAG CAC CCG GGC CTC
ala asp leu STP

1982                                     2012
AGC TGT CTG TGC TGC GAG GGG AGT CTG CCC TGG TGC CCA CTG GGC TGT GGG GTG ACC ACA

2042                                     2072
CTG TAC TTG GGG CTG GGC CCT CTG CCC CTG TGT CCC CAT CTG TGT GCA CTG ATG CTT CCT

2102                                     2132
CCC TTT TTT AAT TTA AAA TGG TTT TTA TAA GCA AAA AAA AAA AAA AAA

```

FIG. 1 (3 of 3)

102101" 8969E/60

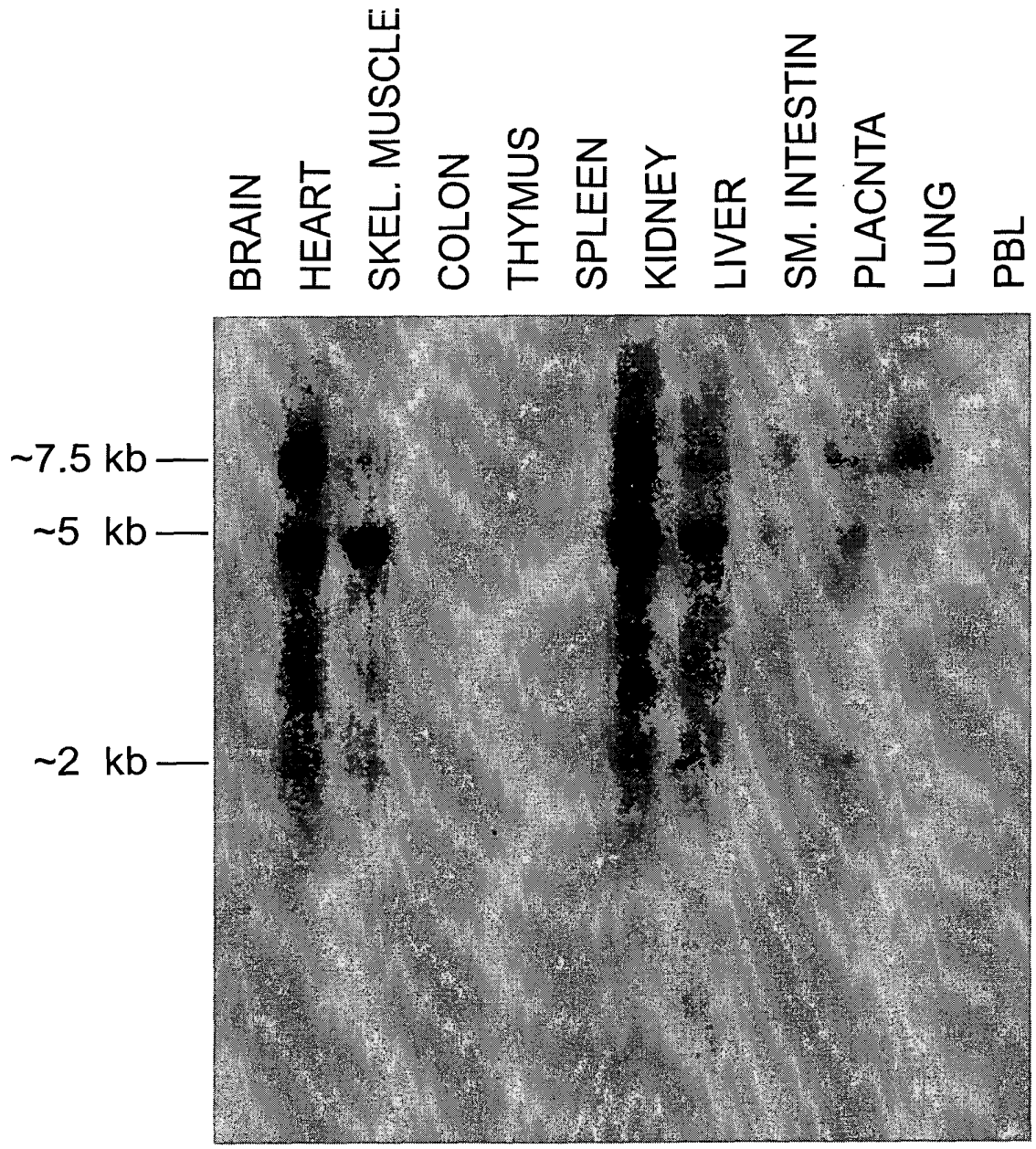


FIG. 2

HC2A	-----
KIAA	ASGNLDKNARFSAIYRQDSNKLSDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	-----
KIAA	FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLYDSQ
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	-----VLHHHQNPFEYDEIK
KIAA	KSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVFTSAFAAVLHHHQNPFEYDEIK
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	IELPTQLHEKHLLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
KIAA	IELPTQLHEKHLLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNNFFQYC
KIAA	PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNNFFQYC
rat	-----
HC4	-----
HC1	-----
HC3	-----GPGPARSTVSIISLISNSARV
HC5	-----
HC2A	QKTESGAQALGNELVKYLKSLHAMEGHVMI AFLPTILNQLFRVLT-RATQEEVAVNVTRV
KIAA	QKTESGAQALGNELVKYLKSLHAMEGHVMI AFLPTILNQLFRVLT-RATQEEVAVNVTRV
rat	-----
HC4	-----MEIQVLIRFLSVILMQLFWLPLNMIHEDDVPISCPMV
HC1	-----MSFLPIILNQLFKVLV-QNEEDEITTTVTRV
HC3	NRSRSLSNSNPDISGTPTPSPDDEVRSIIGSKGLDRSNSWNTGGPKAAPWGSNPSPSAES
HC5	-----

FIG. 3A (1 of 5)

HC2A	I IHVVAQCHEEGLESHLSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSN
KIAA	I IHVVAQCHEEGLESHLSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSN
rat	-----
HC4	LFHIVSKCHEEGLDSYLSSFIKYSFRPGKPSAPQAPLIHETLATMMIALLKQSADFLAIN
HC1	LPDIVAKCHEEQLDHSVQSYIKFVFKTR---ACKERPVEDLAKNVTGLLK-SNDSPTVK
HC3	TQAMDRSCNRMSSHTETSSFLQTLTGRLP----TKKLFHEELALQWVVCSG--SVR---E
HC5	-----
	Cadherin Cleavage
HC2A	KLLRYSWFFFDVLIKSMQHLIENSKVKLIIRNQRFPASYHHAAETVVNMLMPHITQKFGD
KIAA	KLLKYSWFFFDVLIKSMQHLIENSKVKLIIRNQRFPASYHHAVETVVNMLMPHITQKFRD
rat	-----
HC4	KLLKYSWFFFEIIAKSMATYLLLENKIKLTHGQRFPPKAYHHALHSLFLAIT-IVESQYAE
HC1	HVLKHSWFFFAIILKSMQHLIDTNKIQLRPPQRFPESYQNELDNLMVLSHDHVIWKYKD
HC3	SALQQAWFFFELMVKSMVHHLYFNDKLEARKSRFFPERFMDDIAALVSTIASDIVSRFQK
HC5	-----
HC2A	NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDPKTLFEYKFEFL
KIAA	NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDPKTLFEYKFEFL
rat	-----
HC4	IPKESRNVNYSLASFLKCCLTLMDRGFVFNLIN---DYIS--GFSPKDPKVLAEYKFEFL
HC1	ALEETRRATHSVARFLKRCFTFMDRGCVFKMVN---NYIS--MFSSGDLKTLQCQYKFDFL
HC3	DTEMVERLNTSLAFFLNDLLSVMDRGFVFSLIKSCYQVSSKLYSLPNPSVLVSLRLDFL
HC5	-----
HC2A	RVVCNHEHYIPLNLPM-----PFGKGRIQR-----YQDLQL----DYSLTDEF
KIAA	RVVCNHEHYIPLNLPM-----PFGKGRIQR-----YQDLQL----DYSLTDEF
rat	-----
HC4	QTICNHEHYIPLNLPM-----AFAKPKLQR-----VQDSNL----EYSLSDEY
HC1	QEVQCQHEHFIPCLPIRSANIPDPLTPSES-----TQELHASDMPPEYSVTNEF
HC3	RIICSHHEHYVTNLNPLCSLLTPPASPSPSVSSATSQSSGFSTNVQDQKIANMFELS--VPF
HC5	-----MNADTAPTSPCPSIS---SQNSSSCSSSQDQKIASMFDRTSRVP
	Cadherin EC motif
HC2A	CRNHFLVGILLREVG TALQEFRE----VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT
KIAA	CRNHFLVGILLREVG TALQEFRE----VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT
rat	-----
HC4	CKHHFLVGILLRETSIALQDNYE----IRYTAISVIKNLLIKHAFDTRYQHKNQQAQIAQ
HC1	CRKHFLIGILLREVG FALQEDQD----VRHLALAVLKNLMAKHSFDDRYREPRKQAQIAS
HC3	RQQHYLAGIVLTELAVILDPDAEGLFGLHKKVINMVHNLLSSHSDPRYSDPQIKARVAM
HC5	SSTS-SPGILFTELAALDAEGEGISEVQRKAVSAIHSLLSSHDLDPKRCVKPEVKVKIAA
HC2A	LYLPLFGLLIENVQRINVRDVSPPFVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH
KIAA	LYLPLFGLLIENVQRINVRDVSPPFVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH
rat	-----
HC4	LYLPLFVGLLLENIQRLAGRDTLYSCAAMPNSASRDEFPCG-----FTSP--AN--RGSLS
HC1	LYMPYGMLLDNMPRIYKLDLYPFTVNTSNQGSRDDLDSTNGGFQSQTAIKHANSVDTSFS
HC3	LYLPLIGIIMETVPQLYDFTETHNQRGRPICIAATDDYESE-----SG---SMIS
HC5	LYLPLVGII LDALPQLCDFTVADTRRYR---TSGSDEEQE-----GA---GAIT

FIG. 3A (2 of 5)

HHC2A	KDLLGAISGIASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQSS
KIAA	KDLLGAISGIASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQSS
rat	-----
HC4	TDKDTAYGSFQNG-----HGIKREDSRGS LIP-EGATGFPDQNGTGEN-----TRQS
HC1	KDVLNSIAAFSS-----IAISTVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRPL
HC3	QTVAMAIAGTSVPQ-----LTRPGSFLLTSTSGRQHT-----
HC5	QNALAIAGNNFN-----LKTSG-IVLSSLPYKQYN-----
HC2A	TLGNSVVRCDKLDQSEIKSLLMCFLYILKMSDDALFTYWN-KASTSELMDDFFTISEVCL
KIAA	TLGNSVVRCDKLDQSEIKSLLMCFLYILKMSDDALFTYWN-KASTSELMDDFFTISEVCL
rat	-----
HC4	STRSSVSQYNRLDQYEIRSLLMCYLYIVKMISED TLLTYWN-KVSPQELINILILEVCL
HC1	ALIGSTLRFDRLDQAETRSLLMCFLHIMKTISYETLIAYWQ-RAPSPEVSDFFSILDVCL
HC3	-----TFSAESSRSLICLLWVLKN-ADETVLQKWFTDLSVLQNLRLDLLLYLCV
HC5	-----MLNADTTRNLMICFLWIMKN-ADQSLIRKWIADLPSTQLNRILDLLFICV
HC2A	HQFYMGKRYIARNQEGLG--PIVHDRKS-----QTLPVSRNRTGMM
KIAA	HQFYMGKRYIAR-----TGMM
rat	-----
HC4	FHFRYMGRKNIARVHDAWLSKHFGIDRKS-----QTMPALNRNRSGVM
HC1	QNFERYLGKRNIIRKIAAAF--KFVQSTQNNGTLKGSNPSCQTSGLLAQWMHSTSRHEGHK
HC3	SCFEYKGKKVFERMNSLTFK--KSKDMRAK-----LEEAILGSIGARQEMV
HC5	LCFEYKGKQSSDKVSTQVLQ--KSRDVKAR-----LEEALLRGE GARGEMM
HC2A	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
KIAA	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
rat	-----
HC4	QARLQHL-----SSLESS-----FTLNHSSTTTEADIFHQALLEGNTATEVS
HC1	QHRSQTLPIIRGK---NALSNPKL---LQMLDNTMTSNEIDIVHHVDTEANIATEGC
HC3	RRSRGQLERSPSGSAFGSQENLRWRKDMTHWRQNTTEKLDKSRAEIEHEALIDGNLATEAN
HC5	RRRAPGNDRFP-----GLNENLRWKKEQTHWRQANEKLDKTKAELDQEALISGNLATEAH
HC2A	LTALDTLSLFTLAFKNQLLADHGHNPMLKKVFDVYLCFLQKHQSETALKNVFTALRSLIY
KIAA	LTALDTLSLFTLAFKNQLLADHGHNPMLKKVFDVYLCFLQKHQSETALKNVFTALRSLIY
rat	-----KLSRGHSPLMKKVF DVYLCFLQKHQSEMA LKNVFTALRSLIY
HC4	LTVLDTISFFTQCFKTHFLNNDGHNPMLKKVFDIHLAFLKNGQSEVSLKHVFASLRAFIS
HC1	LTILDVLSLFTQTHQRQLQCCDCQNSLMKRGFDTYMLFFQVQNQSATALKHVFASLRLFVC
HC3	LIILDTLEIVQTVS--VTES--KESILGGVLKVLLHSMACNQSAVYLQHC FATQRALVS
HC5	LIILDMQENIIQASS--ALDC--KDSLLGGVLRVLVNSLNC DQSTTYLTHCFATLRALIA
HC2A	KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKS FVRTH
KIAA	KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKS FVRTH
rat	KFPSTFYEGRADMCALCYEVLKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKS FVRTH
HC4	KFPSAFFKGRVNMCAAFCYEVLKCCTSKISSRNEASALLYLLMRNNFEYTKRKTFLRTH
HC1	KFPSAFFQGPADLCGSFCYEVLKCCNHRSRSTQTEASALLYLFMRKNFEFNKQKSIVRSH
HC3	KFPELLFEEETEQCADLCLRLLRHCSSSIGTIRSHPSASLYLLMRQNFEIGN--NFARVK
HC5	KFGDLLFEEEEVEQCFDLCHQVLHHCSSMDVTRSQACATLYLLMRFSFGATS--NFARVK
HC2A	LQVIISVSQLIADVVGIGETRQQSLSIINN CANSRDLIKHTSFSSDVKDLTKRIRTVLM
KIAA	LQVIISVSQLIADVVGIGETRQQSLSIINN CANSRDLIKHTSFSSDVKDLTKRIRTVLM
rat	LQVIISLSQLIADVVGIGETRQQSLSIINN CANSRDLIKHTSFSSDVKDLTKRIRTVLM
HC4	LQIIIAVSQLIADVALSGGSRFQESLFIINN FANS DRPMLARAFPAEVKDLTKRIRTVLM
HC1	LQLIKAVSQLIAD-AGIGGSRFQHSLAITNNFANGDKQMKN SNFPAEVKDLTKRIRTVLM
HC3	MQVPMSLSSSLVGT SQNFNEEFLRRSLKTI LTYAEEDLELRETTFPDQVQDLVFNLMHILS
HC5	MQVTMSLASLVGRAPDFNEEHLRRSLR TILAYSEEDTAMQMTFPPTQVEELLCNLNSILY

FIG. 3A (3 of 5)

Transmembrane

HC2A	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKN GDLSEAAMCYVHV
KIAA	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKN GDLSEAAMCYVHV
rat	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKN GDLSEAAMCYVHV
HC4	ATAQMKEHEKDPEMLIDLQYSLAKSYASTPELRKTWLD SMAKIHVKN GDFSEAAMCYVHV
HC1	ATAQMKEHEKDPEMLVDLQYSLANSYASTPELRRTWLESMAKIHARNGDLSEAAMCYIHI
HC3	DTVKMKEHQEDPEMLIDL MYRIAKGYQTSPDLRLTWLQNMAGKHSERSN HAEAAQCLVHS
HC5	DTVKMREFQEDPEMLMDL MYRIAKSYQASPDRLRLTWLQNMAEKHTKKKCYTEAAMCLVHA

SH3

HC2A	TALVAEYLTRKGV-----	FRQGCTAFRVITPN
KIAA	TALVAEYLTRKEA-----	VQWEPPLLPHSHSACLRRSRGGVFRQGCTAFRVITPN
rat	TALVAEYLTRKEAD-----	LALQREPPVPFYSHTSCQRKSRGGMFRQGCTAFRVITPN
HC4	AALVAEFLHRKKL-----	FPNGCSAFKKITPN
HC1	AALIAEYLKRKG YWKVEIKTASLLSEDPHPCDSNSLLTTPSGGSMFSGWPAFLSITPN	
HC3	AALVAEYLSMLED-----	RKYLPGVCVTFQNISSN
HC5	AALVAEYLSMLED-----	HSYLPVGSVSFQNISSN

ITAM

HC2A	IDEEASMMEDVGMQD-----	VHFNEVDLMELLEQCADGLWKAERYELIADIYKLIIP
KIAA	IDEEASMMEDVGMQD-----	VHFNEVDLMELLEQCADGLWKAERYELIADIYKLIIP
rat	IDEEASMMEDVGMQD-----	VHFNEVDLMELLEQCADGLWKAERLRAGLLTSINSSSP
HC4	IDEEGAMKEDAGMMD-----	VHYSEEV LLELLEQCVNGLWKAERYEITSEISKLIGPI
HC1	IKEEGAAKEDSGMHD-----	TPYNENILVEQLYMCGEFLWKSERYELIADVNKPIIAV
HC3	VLEESAVSDDVSPDEEGICSGKYFTESGLVGLLEQAAASF SMAGMYEAVNEVYKVLIP	
HC5	VLEESVSEDTLSPDEDGVCAGQYFTESGLVGLLEQAAELFSTGGLYETVNEVYKVLIP	

ITAM ITAM

ITAM

ITAM

HC2A	YEKRRD-----	
KIAA	YEKRRD FERLAHL YDTLHRAYSKVTEVMHSGRLLGT YFRVAFFGQAAQYQFTDSETDVE	
rat	SMKSGGTLETTHLYDTLH RPYSKVTEVITR-----	AAGSWDLLPGGLFGQ
HC4	YENRREFENLTQVYRTIHGA YTKILEVMHTKKRLG-----	TFFRVAFYFGQ
HC1	FEKQRDFKKLSDIYYDIHRSY LKVAE VVNSEKRLFG-----	RYFRVAFYFGQ
HC3	HEANRDAKKLSTIHGKLQEA FSKIVHQSTGWERMFG-----	TYFRVGFYFG-
HC5	LEAHREFRKLTLTHSKLQRA FDSIVNKH--KRMFG-----	TYFRVGFFG-

ITAM

ITAM

HC2A	-FFEDEDGKBYIYKEPKLTPLSEISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYA
KIAA	GFFEDEDGKBYIYKEPKLTPLSEISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYA
rat	GFFEDEDGKBYIYKEPKLTPLSEISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLDSKFA
HC4	SFFEEDDGKBYIYKEPKLTGLSEISRLRLVKLYGEKFGTENVKIIQSDSKVNAPKLDPKYA
HC1	GFFEEEEGKBYIYKEPKLTGLSEISQRLLKLYADKFGADNVKIIQDSNKNVNPKDLDPKYA
HC3	TKFGDLDEQBFVYKEPAITKLAEISHRLEGFYGERFGEDVVEVIKDSNPVDKCKLDPNKA
HC5	SKFGDLDEQBFVYKEPAITKLPEISHRLEAFYGC FGAEFVEVIK DSTPVDKTKLDPNKA

ITAM

HC2A	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA
KIAA	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA
rat	YIQVTHVTPFFDEKELQERKTEFERCHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA
HC4	HIQVTVVKPYFDDKELTERKTEFERNHNISRFVFEAPYTLSGKKQGCIEEQCKRRTILT
HC1	YIQVTVVTPFFEEKEIEDRKTD FEMHHNINRFVFETPFTLSGKKHGGVAEQCKRRTILT
HC3	YIQITVVEPYFDTYEMKDRITYFDKNYNLRRFMYCTPFTLDGRAHGEHQFKRKITILT
HC5	YIQITVVEPYFDEYEMKDRVITYFEKNFNLRRFMYTTPFTLEGRPRGELHEQYRRNTVLT

FIG. 3A (4 of 5)



		Coiled-Coil 1
HC2A	IHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELRQLC	SSAEVDMIKLQLKLQGSV
KIAA	IHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELRQLC	SSAEVDMIKLQLKLQGSV
rat	IHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELHQLC	SSAEVDMIKLQLKLQGSV
HC4	SNSFPYVKKRIPINCEQQINLKPIDGATDEIKDKTAEHQKCS	STDVDMIQKLKLQGSV
HC1	SHLFPYVKKRIQVISQSSTELNPIEVAIDEMSRKVSELNQLCT	MEEVDMISLQLKLQGSV
HC3	SHAFPIKTRVNVTHKEEIIILTPIEVAIEDMQKKTQELAFATHQ	DPADPKMLQMVQLQGSV
HC5	MHAFPIKTRISVIQKEEFVLTPIEVAIEDMKKKTLQLAVAINQE	PPDAKMLQMVQLQGSV
		Coiled-Coil 2
HC2A	SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEAC	QALAVNERLIKEDQLE
KIAA	SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEAC	QALAVNERLIKEDQLE
rat	SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEAC	QALAVNERLIKEDQLE
HC4	SVQVNAGPLAYARAFLLDSQASKYPPKKVSELKDMFRKFIQACS	IALELNERLIKEDQVE
HC1	SVKVNAGPMAYARAFLEETNAKKYPDNQVKLLKEIFRQFADACG	QALDVNERLIKEDQLE
HC3	GTTVNQGPLEVAQVFLSEIPSDPKLFRHHNKLRLCFKDFTKRC	EDALRNKSLIGPVQKE
HC5	GATVNQGPLEVAQVFLAEIPADPKLYRHHNKLRLCFKEFIMRC	GEAVEKNKRLITADQRE
		Coiled-Coil 2
HC2A	YQEEMKANYREMAKELSEIMHEQICPLEEKTS-VLPNSLHIFNA	ISGTPSTMTVHGMTSS
KIAA	YQEEMKANYREMAKELSEIMHEQLG-----	
rat	YQEEMKANYREIRKELSDIIVPRICPGEDKRAKTFPAHLQRHQ	RDTNKHSGSRVDQFILS
HC4	YHEGLKSNFRDMVKELSDIIEHQILQEDTMHSPWMSNTLHVFC	AISGTSSDRGYGSPRYA
HC1	YQEELRSHYKMDLSELSTVMNEQITGRDDLSK---RGVDQTCT	RVISKATPALPTVSISS
HC3	YQRELG---KLSS-----P-----	
HC5	YQELKKNYNKLKENLRPMIERKIPELYKPIFRVESQKRDSFHR	SSFRKCETQLSQGS--
	PBM	
HC2A	SSVV-----	
KIAA	-----	
rat	CVTLPHPEPHVGTCTFVMCKLRTTFRANHWFCQAQEEAMGNG	REKEPWTVIFNSRFYRSWKG
HC4	EV-----	
HC1	SAEV-----	
HC3	-----	
HC5	-----	
HC2A	-----	
KIAA	-----	
rat	VHIF	
HC4	-----	
HC1	-----	
HC3	-----	
HC5	-----	

FIG. 3A (5 of 5)

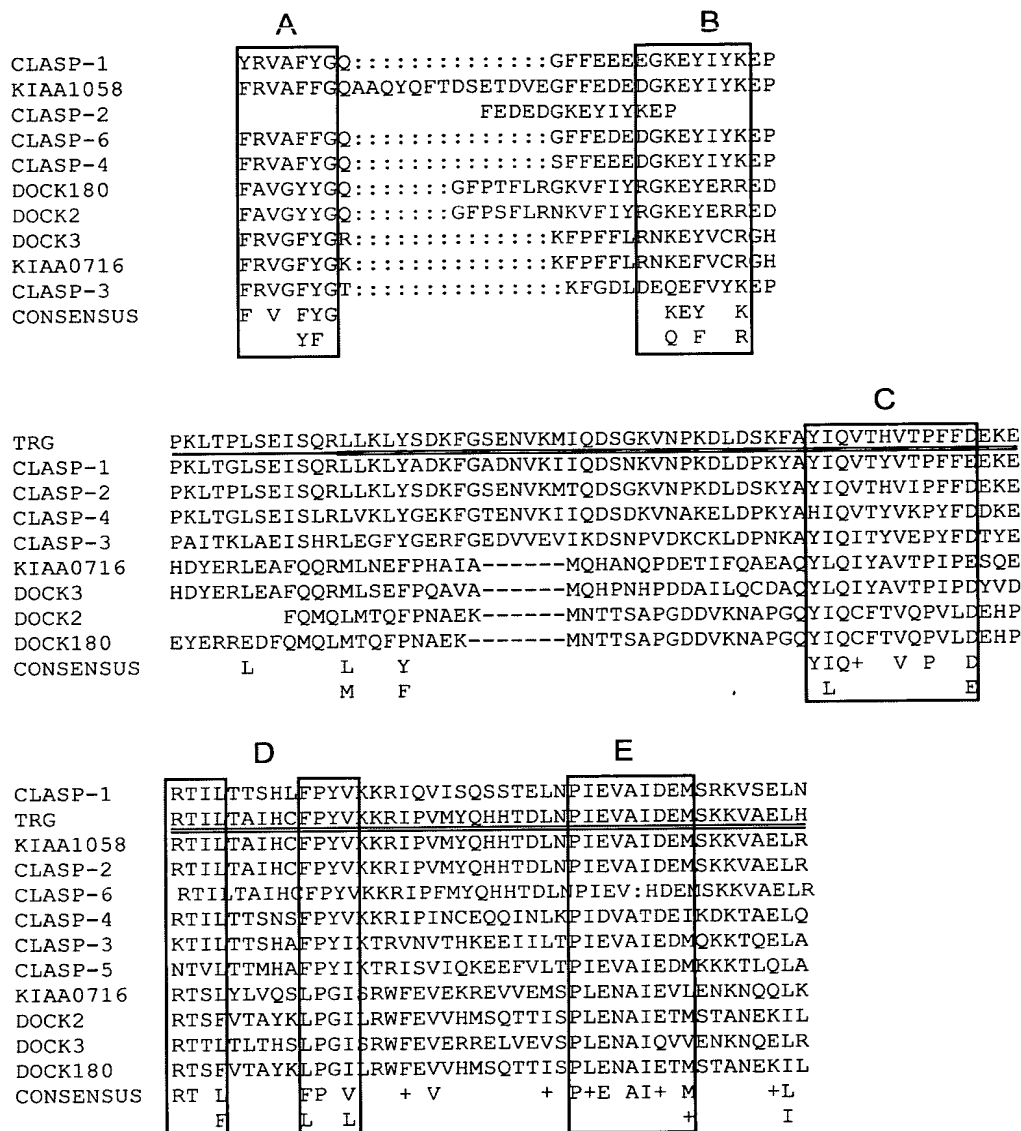


FIG. 3B (1 of 2)



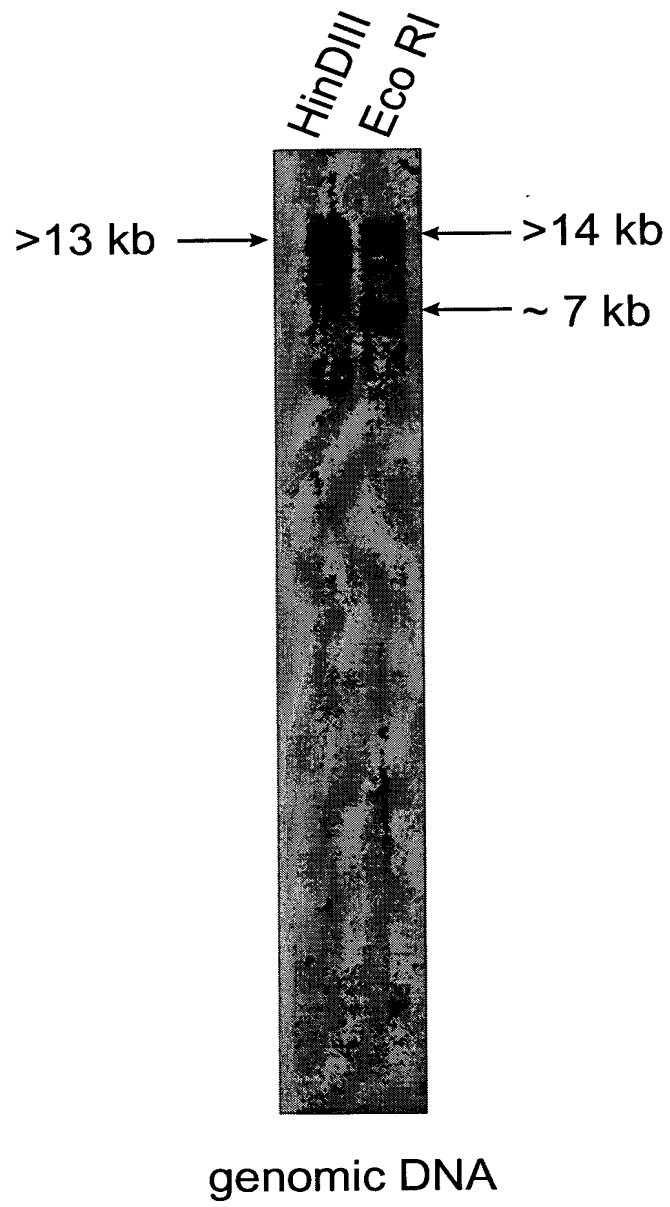


FIG. 4

-12                    -1  
GACGCGAGGACC

1/1	31/11
ATG GCT GCC TCC GAG CGC CGC GCC TTC GCG	CAC AAG ATC AAC AGG ACG GTG GCC GCA GAG
Met ala ala ser glu arg arg ala phe ala	his lys ile asn arg thr val ala ala glu
61/21	91/31
GTG CGG AAG CAG GTG TCC CGG GAA CGC AGT	GGC TCC CCC CAC TCC AGC AGG CGC TGC AGC
val arg lys gln val ser arg glu arg ser	gly ser pro his ser ser arg arg cys ser
121/41	151/51
AGC TCC CTG GGG GTC CCA CTG ACT GAA GTT	GTC GAG CCC CTG GAC TTT GAG GAT GTA CTT
ser ser leu gly val pro leu thr glu val	val glu pro leu asp phe glu asp val leu
181/61	211/71
CTG AGC CGG CCA CCA GAT GCT GAG CCC GGG	CCC CTC AGG GAC CTG GTA GAA TTC CCA GCT
leu ser arg pro pro asp ala glu pro gly	pro leu arg asp leu val glu phe pro ala
241/81	271/91
GAT GAC TTG GAG CTG CTG CTG CAG CCC CGG	GAA TGC CGG ACC ACG GAG CCC GGG ATC CCC
asp asp leu glu leu leu leu gln pro arg	glu cys arg thr thr glu pro gly ile pro
301/101	331/111
AAG GAT GAA AAA CTG GAT GCC CAG GTG AGG	GCC GCG GTG GAG ATG TAT ATT GAG GAC TGG
lys asp glu lys leu asp ala gln val arg	ala ala val glu met tyr ile glu asp trp
361/121	391/131
GTC ATT GTC CAC AGA AGG TAT CAG TAC CTG	AGT GCA GCA TAC AGC CCC GTC ACC ACA GAC
val ile val his arg arg tyr gln tyr leu	ser ala ala tyr ser pro val thr thr asp
421/141	451/151
ACA CAG CGG GAG CGA CAG AAG GGC CTC CCC	CGC CAG GTC TTT GAG CAG GAT GCT TCT GGA
thr gln arg glu arg gln lys gly leu pro	arg gln val phe glu gln asp ala ser gly
481/161	511/171
GAC GAG AGG TCC GGC CCT GAG GAC TCG AAT	GAC TCC CGG CGT GGC TCG GGC TCC CCG GAA
asp glu arg ser gly pro glu asp ser asn	asp ser arg arg gly ser gly ser pro glu
541/181	571/191
GAC ACC CCT CGA AGC AGT GGT GCC TCT AGC	ATC TTC GAC CTG AGG AAC CTG GCA GCT GAC
asp thr pro arg ser ser gly ala ser ser	ile phe asp leu arg asn leu ala ala asp
601/201	631/211
TCA TTG CTG CCC TCT CTG CTA GAG CGG GCG	GCC CCA GAA GAT GTG GAC CGG CGC AAT GAA
ser leu leu pro ser leu leu glu arg ala	ala pro glu asp val asp arg arg asn glu
661/221	691/231
ACC CTT CGA CGG CAG CAC CGG CCC CCG GCC	CTG CTC ACC CTC TAC CCG GCA CCT GAC GAG
thr leu arg arg gln his arg pro pro ala	leu leu thr leu tyr pro ala pro asp glu
721/241	751/251
GAT GAA GCC GTG GAA CGC TGT AGC CGC CCA	GAG CCA CCC CGC GAG CAC TTT GGA CAA AGG
asp glu ala val glu arg cys ser arg pro	glu pro pro arg glu his phe gly gln arg
781/261	811/271
ATC TTG GTC AAG TGT CTG TCG CTC AAG TTC	GAG ATT GAA ATT GAG CCC ATC TTT GGG ATC
ile leu val lys cys leu ser leu lys phe	glu ile glu ile glu pro ile phe gly ile
841/281	871/291
TTG GCT CTG TAT GAT GTG CGG GAG AAA AAG	AAG ATC TCG GAG AAC TTC TAC TTC GAC CTG
leu ala leu tyr asp val arg glu lys lys	lys ile ser glu asn phe tyr phe asp leu
901/301	931/311
AAC TCG GAC TCC ATG AAG GGG CTG CTT CGG	GCT CAT GGC ACC CAC CCT GCC ATC TCC ACC
asn ser asp ser met lys gly leu leu arg	ala his gly thr his pro ala ile ser thr
961/321	991/331
CTG GCC CGC TCT GCC ATC TTC TCT GTG ACC	TAC CCC TCA CCT GAC ATC TTC CTG GTC ATC
leu ala arg ser ala ile phe ser val thr	tyr pro ser pro asp ile phe leu val ile
1021/341	1051/351
AAG TTG GAG AAG GTG CTT CAG CAA GGG GAC	ATC AGT GAG TGC TGT GAG CCT TAC ATG GTG
lys leu glu lys val leu gln gln gly asp	ile ser glu cys cys glu pro tyr met val
1081/361	1111/371
TTG AAA GAA GTG GAC ACA GCC AAG AAC AAA	GAG AAG CTA GAG AAG CTG CGC CTG GCG GCC
leu lys glu val asp thr ala lys asn lys	glu lys leu glu lys leu arg leu ala ala

09736966-101201

FIG. 5A (1 of 6)

1141/381	GAG CAG TTC TGC ACC CGC CTG GGC CGC TAC	1171/391	CGC ATG CCC TTC GCC TGG ACG GCC GTG CAC
1201/401	glu gln phe cys thr arg leu gly arg tyr	1231/411	arg met pro phe ala trp thr ala val his
1261/421	TTG GCC AAC ATC GTG AGC AGC GCT GGG CAG	1291/431	CTG GAC CGG GAC TCT GAC TCG GAG GGC GAG
1321/441	leu ala asn ile val ser ser ala gly gln	1351/451	leu asp arg asp ser asp ser glu gly glu
1381/461	CGC CGG CCA GCC TGG ACA GAC CGC CGC CGT	1411/471	CCA GCC ACG CTA ACT GTC ACA AAC TTC TTT
1441/481	arg arg pro ala trp thr asp arg arg arg	1471/491	pro ala thr leu thr val thr asn phe phe
1501/501	GAC GAC GCC TGC AGC TTC TCT GGC TTC CGT	1531/511	GAC CTC TTC AAG TTC CTG GCT GAC ATG AGG
1561/521	AAG CAG GAG GCT GAG CGA CTC AGT GAC GAG	1591/531	asp leu phe lys phe leu ala asp met arg
1621/541	CGC CCG TCG TCC CTG CTG CGG CGA CTA CGT	1651/551	CCT GTG ACT GCC CAG CTC AAG ATC GAC ATT
1681/561	arg pro ser ser leu leu arg arg leu arg	1711/571	pro val thr ala gln leu lys ile asp ile
1741/581	TCT CCG GCT CCT GAA AAT CCC CAC TTC TGC	1771/591	CTC TCC CCT GAG CTG CTT CAT ATC AAG CCC
1801/601	TAC CCG GAC CCC AGG GGC CGG CCC ACC AAG	1831/611	leu ser pro glu leu leu his ile lys pro
1861/621	tyr pro asp pro arg gly arg pro thr lys	1891/631	GAG ATT CTG GAG TTC CCC GCC CGC GAA GTC
1921/641	TAT GCC CCC CAT ACC AGC TAC AGG AAC CTG	1951/651	glu ile leu glu phe pro ala arg glu val
1981/661	AGC AGC CGC CAG GGC TCC GTG CGC AAC CTT	2011/671	CTG TAC GTG TAC CCG CAC AGC CTC AAC TTC
2041/681	ser ser arg gln gly ser val arg asn leu	2071/691	leu tyr val tyr pro his ser leu asn phe
2101/701	GAC CCC AGC CAG GCT CTG CCG GTC ATC TTT	2131/711	GCT GTG CGA GTG CAG TAC ATG ACA GGC GAG
2161/721	asp pro ser gln ala leu pro val ile phe	2191/731	ala val arg val gln tyr met thr gly glu
2221/741	CTG CTG CAG CAC GGG CGC CTG AGG ACC GGC	2251/751	GGC AAG TCC AGC TGC AGT GAA TTT ACC CGC
	leu leu gln his gly arg leu arg thr gly		gly lys ser ser cys ser glu phe thr arg
	CGG CCG CCC AGC TAT TCC GTG CTC ACA CCC		AAG TCC CCC GAG TTC TAC GAG GAG TTC AAG
	pro pro pro ser tyr ser val leu thr pro		lys ser pro glu phe tyr glu glu phe lys
	GAC GGT CAC AAG GGC GTG TTC AGT GTG GAG		CAT CAC CTG CTG TTC ACC TTC TAC CAT GTC
	asp gly his lys gly val phe ser val glu		his his leu leu phe thr phe tyr his val
	GAC CCC TAC CTG GAC AAA TTC TTC ACC CTG		GAG ACA CCC GTG GGC TTT ACT TGG ATC CCA
	asp pro tyr leu asp lys phe phe thr leu		glu thr pro val gly phe thr trp ile pro
	TTC CGG CTC AAG GAC ACT GTG CTG AGC GAG		CCC TTC TGT CTC CCA GTG TCT GTG GAC CAG
	phe arg leu lys asp thr val leu ser glu		pro phe cys leu pro val ser val asp gln
			GAT GTG GCG CTT CCG GGC ATG CGC TGG GTG
			asp val ala leu pro gly met arg trp val
			CTC ACA GCC GTG TCC TCT GTG CAC CCC CAG
			leu thr ala val ser ser val his pro gln
			GTG CAC GTC CTG GAG GAG GGA GCC TTC CCA
			val his val leu glu glu gly ala phe pro
			GGC AAC GTG GAG CAG GAG CTG CGG GCC AGT
			gly asn val glu gln glu leu arg ala ser

FIG. 5A (2 of 6)

2281/761	CTT GCA GCA CTG CGC CTG GCC AGC CCC GAA	2311/771	CCC CTT GTG GCC TTC TCC CAC CAC GTG CTG
leu ala ala leu arg leu ala ser pro glu	pro leu val ala phe ser his his val leu		
2341/781	GAC AAG CTC GTG CGT CTG GTC ATC AGG CCC	2371/791	CCG ATC ATC AGT GGC CAG ATT GTG AAC CTG
asp lys leu val arg leu val ile arg pro	pro ile ile ser gly gln ile val asn leu		
2401/801	GGC CGT GGA GCC TTT GAA GCA ATG GCC CAT	2431/811	GTA GTC AGC CTT GTT CAC CGG AGC CTG GAG
gly arg gly ala phe glu ala met ala his	val val ser leu val his arg ser leu glu		
2461/821	GCA GCC CAG GAT GCC CGC GGT CAC TGC CCA	2491/831	CAG CTG GCT GCC TAC GTC CAC TAC GCC TTT
ala ala gln asp ala arg gly his cys pro	gln leu ala ala tyr val his tyr ala phe		
2521/841	CGC CTT CCT GGC ACT GAG CCC AGC CTC CCG	2551/851	GAT GGG GCC CCT CCA GTG ACA GTG CAG GCT
arg leu pro gly thr glu pro ser leu pro	asp gly ala pro pro val thr val gln ala		
2581/861	GCC ACA CTG GCC CGT GGC TCT GGT CGC CCC	2611/871	GCA AGC CTC TAC CTG GCG CGT TCC AAG AGC
ala thr leu ala arg gly ser gly arg pro	ala ser leu tyr leu ala arg ser lys ser		
2641/881	ATC AGC AGC AGC AAC CCT GAC CTC GCC GTG	2671/891	GCC CCT GGC TCT GTG GAT GAC GAG GTT TCC
ile ser ser ser asn pro asp leu ala val	ala pro gly ser val asp asp glu val ser		
2701/901	CGC ATC CTG GCC AGC AAG CTG CTT CAC GAG	2731/911	GAG CTG GCT CTG CAG TGG GTG GTC AGC AGC
arg ile leu ala ser lys leu leu his glu	glu leu ala leu gln trp val val ser ser		
2761/921	AGT GCC GTA CGC GAG GCC ATC CTC CAG CAC	2791/931	GCC TGG TTC TTC TTC CAG CTC ATG GTG AAG
ser ala val arg glu ala ile leu gln his	ala trp phe phe phe gln leu met val lys		
2821/941	AGT ATG GCG CTG CAC CTG CTG CTT GGC CAG	2851/951	CGA CTA GAC ACA CCC CGC AAG CTG CGC TTC
ser met ala leu his leu leu leu gly gln	arg leu asp thr pro arg lys leu arg phe		
2881/961	CCC GGA CGC TTC CTG GAC GAC ATC ACT GCC	2911/971	TTG GTG GGC TCT GTG GGC CTG GAG GTC ATC
pro gly arg phe leu asp asp ile thr ala	leu val gly ser val gly leu glu val ile		
2941/981	ACC CGT GTC CAC AAG GAT GTG GAG CTG GCC	2971/991	GAG CAC CTC AAC GCC AGC CTG GCT TTC TTC
thr arg val his lys asp val glu leu ala	glu his leu asn ala ser leu ala phe phe		
3001/1001	CTC AGT GAC CTT CTG TCC CTG GTG GAC CGG	3031/1011	GGC TTT GTC TTC AGC CTG GTC CGG GCC CAC
leu ser asp leu leu ser leu val asp arg	gly phe val phe ser leu val arg ala his		
3061/1021	TAC AAG CAG GTG GCC ACG CGG CTC CAG TCG	3091/1031	TCC CCT AAT CCA GCA GCC CTG CTG ACC CTG
tyr lys gln val ala thr arg leu gln ser	ser pro asn pro ala ala leu leu thr leu		
3121/1041	CGC ATG GAA TTC ACC CGC ATC CTG TGC AGC	3151/1051	CAC GAG CAC TAC GTG ACC CTC AAC CTC CCC
arg met glu phe thr arg ile leu cys ser	his glu his tyr val thr leu asn leu pro		
3181/1061	TGC TGC CCC CTG TCA CCT CCA GCC TCG CCC	3211/1071	TCC CCC TCT GTG TCC TCC ACC ACC TCC CAG
cys cys pro leu ser pro pro ala ser pro	ser pro ser val ser ser thr thr ser gln		
3241/1081	AGC TCC ACC TTC TCC AGC CAA GCC CCG GAC	3271/1091	CCC AAG GTG ACC AGC ATG TTC GAA CTG AGT
ser ser thr phe ser ser gln ala pro asp	pro lys val thr ser met phe glu leu ser		
3301/1101	GGA CCA TTC CGG CAG CAG CAC TTC CTA GCT	3331/1111	GGG CTC CTG CTG ACG GAG CTG GCA CTG GCC
gly pro phe arg gln gln his phe leu ala	gly leu leu leu thr glu leu ala leu ala		
3361/1121	CTC GAA CCT GAG GCT GAA GGG GCA TTC CTG	3391/1131	TTG CAC AAG AAG GCC ATC AGT GCT GTG CAC
leu glu pro glu ala glu gly ala phe leu	leu his lys lys ala ile ser ala val his		
3421/1141	AGC CTG CTA TGT GGC CAT GAC ACT GAC CCC	3451/1151	CGC TAC GCC GAG GCC ACT GTG AAG GCT CGT
ser leu leu cys gly his asp thr asp pro	arg tyr ala glu ala thr val lys ala arg		
3481/1161	GTG GCC GAG CTG TAC CTG CCA CTG CTT TCG	3511/1171	ATT GCA CGG GAT ACC TTG CCA CGG CTG CAT
val ala glu leu tyr leu pro leu leu ser	ile ala arg asp thr leu pro arg leu his		

FIG. 5A (3 of 6)

3541/1181	GAC TTT GCT GAG GGC CCA GGT CAG CGG TCA	3571/1191	AGA CTG GCC TCA ATG CTT GAC TCA GAC ACA
asp phe ala glu gly pro gly gln arg ser		arg leu ala ser met leu asp ser asp thr	
3601/1201		3631/1211	
GAA GGC GAA GGG GAC ATT GCG GGT ACC ATC		AAC CCC TCT GTG GCC ATG GCC ATT GCT GGT	
glu gly glu gly asp ile ala gly thr ile		asn pro ser val ala met ala ile ala gly	
3661/1221		3691/1231	
GGC CCC CTA GCC CCT GGC TCC CGG GCC AGC		ATC TCC CAG GGG CCA CCA ACG GCT TCT CGC	
gly pro leu ala pro gly ser arg ala ser		ile ser gln gly pro pro thr ala ser arg	
3721/1241		3751/1251	
GCA GGC TGT GCC CTC TCT GCT GAG TCA AGC		CGG ACC TTG CTG GCG TGT GTG CTG TGG GTG	
ala gly cys ala leu ser ala glu ser ser		arg thr leu leu ala cys val leu trp val	
3781/1261		3811/1271	
CTG AAA AAC ACC GAG CCG GCG CTC CTG CAG		CGC TGG GCC ACT GAC CTG ACA CTC CCC CAG	
leu lys asn thr glu pro ala leu leu gln		arg trp ala thr asp leu thr leu pro gln	
3841/1281		3871/1291	
CTG GGA CGT CTG TTG GAC TTG CTG TAC CTT		TGC CTG GCT GCC TTT GAG TAC AAG GGG AAA	
leu gly arg leu leu asp leu leu tyr leu		cys leu ala ala phe glu tyr lys gly lys	
3901/1301		3931/1311	
AAG GCC TTT GAA CGC ATC AAC AGC CTC ACA		TTC AAA AAA TCT CTG GAT ATG AAG GCG CGG	
lys ala phe glu arg ile asn ser leu thr		phe lys lys ser leu asp met lys ala arg	
3961/1321		3991/1331	
CTA GAG GAA GCC ATT CTG GGT ACC ATC GGA		GCT CGA CAA GAA ATG GTT CGG CGA AGT CGT	
leu glu glu ala ile leu gly thr ile gly		ala arg gln glu met val arg arg ser arg	
4021/1341		4051/1351	
GAG AGG AGC CCG TTT GGG AAT CCA GAG AAC		GTG CGC TGG CGG AAG AGC GTC ACA CAC TGG	
glu arg ser pro phe gly asn pro glu asn		val arg trp arg lys ser val thr his trp	
4081/1361		4111/1371	
AAG CAA ACC TCA GAC CGC GTG GAC AAG ACC		AAG GAT GAA ATG GAA CAC GAG GCC TTG GTG	
lys gln thr ser asp arg val asp lys thr		lys asp glu met glu his glu ala leu val	
4141/1381		4171/1391	
GAA GGG AAC CTG GCA ACC GAG GCA AGC CTA		GTG GTT CTG GAC ACA CTG GAG ATC ATC GTG	
glu gly asn leu ala thr glu ala ser leu		val val leu asp thr leu glu ile ile val	
4201/1401		4231/1411	
CAG ACG GTG ATG CTT TCA GAA GCC CGG GAG		AGC GTC TTG GGG GCA GTG CTG AAG GTT GTG	
gln thr val met leu ser glu ala arg glu		ser val leu gly ala val leu lys val val	
4261/1421		4291/1431	
CTG TAC AGC CTG GGC AGT GCC CAG AGT GCC		CTC TTC TTG CAG CAT GGC CTG GCC ACC CAG	
leu tyr ser leu gly ser ala gln ser ala		leu phe leu gln his gly leu ala thr gln	
4321/1441		4351/1451	
AGG GCC CTT GTG TCC AAG TTC CCG GAG CTG		CTG TTC GAG GAG GAC ACG GAG CTG TGT GCC	
arg ala leu val ser lys phe pro glu leu		leu phe glu glu asp thr glu leu cys ala	
4381/1461		4411/1471	
GAC CTG TGC CTG AGG CTC CTA CGA CAC TGT		GGC AGC CGC ATC AGC ACC ATC CGC ACG CAC	
asp leu cys leu arg leu leu arg his cys		gly ser arg ile ser thr ile arg thr his	
4441/1481		4471/1491	
GCC AGC GCC TCG CTG TAC CTG CTC ATG CGA		CAG AAC TTC GAG ATC GGC CAC AAC TTT GCC	
ala ser ala ser leu tyr leu leu met arg		gln asn phe glu ile gly his asn phe ala	
4501/1501		4531/1511	
CGT GTG AAG ATG CAG GTC ACC ATG TCT CTC		TCG TCC CTG GTG GGG ACG ACG CAG AAC TTC	
arg val lys met gln val thr met ser leu		ser ser leu val gly thr thr gln asn phe	
4561/1521		4591/1531	
AGT GAA GAG CAC CTG CGA CGT TCA CTC AAA		ACC ATC CTC ACC TAT GCT GAG GAG GAC ATG	
ser glu glu his leu arg arg ser leu lys		thr ile leu thr tyr ala glu glu asp met	
4621/1541		4651/1551	
GGG CTG CGG GAC AGC ACC TTC GCA GAG CAG		GTC CAG GAC CTG ATG TTC AAC CTG CAC ATG	
gly leu arg asp ser thr phe ala glu gln		val gln asp leu met phe asn leu his met	
4681/1561		4711/1571	
ATC CTG ACG GAC ACG GTG AAG ATG AAG GAA		CAC CAG GAG GAC CCT GAG ATG CTC ATC GAC	
ile leu thr asp thr val lys met lys glu		his gln glu asp pro glu met leu ile asp	

FIG. 5A (4 of 6)



4741/1581	CTC ATG TAC AGA ATT GCC CGG GGC TAC CAG	4771/1591	GGC TCA CCG GAC CTT CGG CTG ACC TGG TTG
leu met tyr arg ile ala arg gly tyr gln		gly ser pro asp leu arg leu thr trp leu	
4801/1601	CAG AAC ATG GCC GGG AAG CAC GCG GAG CTG	4831/1611	GGC AAC CAC GCC GAG GCC GCC CAG TGC ATG
gln asn met ala gly lys his ala glu leu		gly asn his ala glu ala ala gln cys met	
4861/1621	GTG CAC GCG GCC GCC CTC GTG GCT GAG TAC	4891/1631	CTC GCC CTG CTC GAG GAC CAG CGC CAC CTG
val his ala ala ala leu val ala glu tyr		leu ala leu leu glu asp gln arg his leu	
4921/1641	CCC GTG GGC TGC GTT TCC TTC CAG AAC ATC	4951/1651	TCA TCC AAC GTG CTA GAG GAG TCC GCC ATC
pro val gly cys val ser phe gln asn ile		ser ser asn val leu glu glu ser ala ile	
4981/1661	TCC GAC GAC ATC CTG TCG CCC GAC GAG GAG	5011/1671	GGC TTC TGC TCC GGG AAG CAC TTC ACT GAG
ser asp asp ile leu ser pro asp glu glu		gly phe cys ser gly lys his phe thr glu	
5041/1681	CTG GGG CTG GTA GGG TTG CTG GAA CAG GCA	5071/1691	GCC GGC TAC TTC ACC ATG GGC GGG CTC TAC
leu gly leu val gly leu leu glu gln ala		ala gly tyr phe thr met gly gly leu tyr	
5101/1701	GAG GCG GTG AAT GAG GTC TAC AAG AAC CTC	5131/1711	ATC CCC ATC CTG GAA GCC CAC CGT GAC TAC
glu ala val asn glu val tyr lys asn leu		ile pro ile leu glu ala his arg asp tyr	
5161/1721	AAG AAG CTG GCC GCG GTG CAC GGC AAA CTG	5191/1731	CAG GAG GCC TTC ACC AAG ATC ATG CAC CAG
lys lys leu ala ala val his gly lys leu		gln glu ala phe thr lys ile met his gln	
5221/1741	AGT TCC GGC TGG GAG CGC GTG TTC GGG ACG	5251/1751	TAT TTC CGC GTG GGC TTC TAC GGC GCC CAC
ser ser gly trp glu arg val phe gly thr		tyr phe arg val gly phe tyr gly ala his	
5281/1761	TTC GGT GAC CTG GAT GAG CAG GAG TTT GTG	5311/1771	TAC AAG GAG CCA TCG ATC ACG AAG CTG GCA
phe gly asp leu asp glu gln glu phe val		tyr lys glu pro ser ile thr lys leu ala	
5341/1781	GAG ATC TCA CAC CGG CTG GAG GAG TTC TAC	5371/1791	ACG GAG AGA TTT GGC GAC GAC GTC GTT GAG
glu ile ser his arg leu glu glu phe tyr		thr glu arg phe gly asp asp val val glu	
5401/1801	ATT ATC AAA GAC TCT TAC CCT GTG GAC AAG	5431/1811	TCC AAG CTT GAC TCA CAA AAG GCC TAC ATC
ile ile lys asp ser tyr pro val asp lys		ser lys leu asp ser gln lys ala tyr ile	
5461/1821	CAG ATC ACG TAT GTG GAA CCG TAC TTT GAT	5491/1831	ACC TAC GAG CTC AAG GAC CGG GTG ACC TAC
gln ile thr tyr val glu pro tyr phe asp		thr tyr glu leu lys asp arg val thr tyr	
5521/1841	TTT GAC CGC AAC TAT GGG CTT CGC ACA TTC	5551/1851	CTG TTC TGC ACG CCG TTC ACG CCG GAT GGG
phe asp arg asn tyr gly leu arg thr phe		leu phe cys thr pro phe thr pro asp gly	
5581/1861	CGC GCA CAC GGG GAG CTG CCC GAG CAA CAC	5611/1871	AAG CGT AAG ACG CTG CTC AGC ACC GAC CAC
arg ala his gly glu leu pro glu gln his		lys arg lys thr leu leu ser thr asp his	
5641/1881	GCC TTC CCC TAC ATC AAG ACT CGC ATC CGT	5671/1891	GTG TGC CAC CGG GAG GAG ACG GTG CTG ACG
ala phe pro tyr ile lys thr arg ile arg		val cys his arg glu glu thr val leu thr	
5701/1901	CCA GTG GAG GTG GCC ATC GAG GAC ATG CAG	5731/1911	AAG AAG ACA CGG GAG CTG GCC TTT GCC ACC
pro val glu val ala ile glu asp met gln		lys lys thr arg glu leu ala phe ala thr	
5761/1921	GAG CAG GAC CCA CCA GAT GCT AAG ATG CTA	5791/1931	CAG ATG GTG CTT CAG GGC TCT GTA GGG CCC
glu gln asp pro pro asp ala lys met leu		gln met val leu gln gly ser val gly pro	
5821/1941	ACC GTG AAC CAG GGT CCC CTG GAG GTG GCC	5851/1951	CAG GTG TTT TTA GCA GAG ATC CCG GAA GAC
thr val asn gln gly pro leu glu val ala		gln val phe leu ala glu ile pro glu asp	
5881/1961	CCC AAG CTC TTC CGG CAT CAC AAC AAA TTG	5911/1971	CGG CTC TGC TTC AAG GAC TTC TGC AAG AAA
pro lys leu phe arg his his asn lys leu		arg leu cys phe lys asp phe cys lys lys	

FIG. 5A (5 of 6)

5941/1981	5971/1991
TGT GAG GAT GCG CTG CGG AAA AAT AAG GCC	CTG ATT GGG CCG GAC CAG AAG GAG TAC CAC
cys glu asp ala leu arg lys asn lys ala	leu ile gly pro asp gln lys glu tyr his
6001/2001	6031/2011
CGT GAG CTG GAG CGC AAC TAC TGC CGC CTG	CGG GAG GCT CTG CAG CCC CTG CTT ACC CAG
arg glu leu glu arg asn tyr cys arg leu	arg glu ala leu gln pro leu leu thr gln
6061/2021	6091/2031
CGC CTG CCC CAG CTG ATG GCA CCC ACC CCA	CCC GGC CTC AGG AAC TCC TTG AAC AGA GCA
arg leu pro gln leu met ala pro thr pro	pro gly leu arg asn ser leu asn arg ala
6121/2041	6151/2051
AGT TTC CGA AAG GCA GAC CTC TGA GCC CAC	AAG GAC CAA AGC TGT ACC TAG AGG AAC CAG
ser phe arg lys ala asp leu OPA	
6181/2061	6211/2071
CAC CCG GGC CTC AGC TGT CTG TGC TGC GAG	GGG AGT CTG CCC TGG TGC CCA CTG GGC TGT
6241/2081	6271/2091
GGG GTG ACC ACA CTG TAC TTG GGG CTG GGC	CCT CTG CCC CTG TGT CCC CAT CTG TGT GCA
6301/2101	6331/2111
CTG ATG CTT CCT CCC TTT TTT AAT TTA AAA	TGG TTT TTA TAA GCA AAA AAA AAA AAA AAA

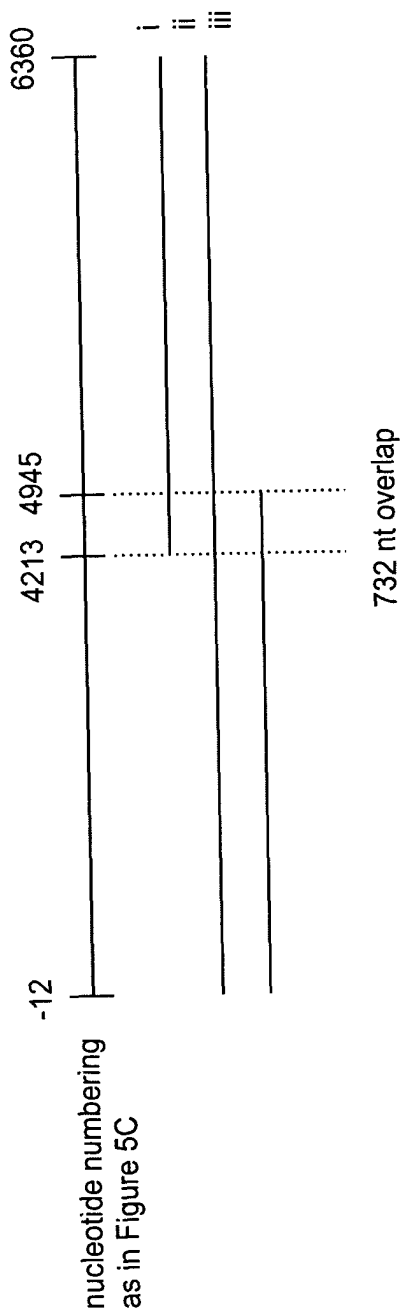
FIG. 5A (6 of 6)

A. Allelic variations: single nucleotide changes (polymorphism) between CLASP-7 cDNA isoforms

Isoform	Nucleotide(s)	Consequence
1	1993	G to A; glycine to arginine
2	2136	A to G; missense
3	3166	A to G; threonine to alanine
4	3902	A to T; lysine to methionine
5	3918	C to T; missense
6	3937	A to C; lysine to glutamine
7	4002	A to C; glutamic acid to aspartic acid
8	4017	T to A; serine to arginine
9	4020	T to C; missense
10	4034-5	TT to AC; phenylalanine to tyrosine
11	4911	G to C change; missense mutation changing codon from glutamine to histidine

These differences may be found separately or together in various combination in the difference human CLASP-7 isoforms

FIG. 5B (2 of 2)



Exon 63800 to 63920

GCGGGGCCGGGGCCCCGGGGCGGGCGGGCGGGACGCGAGGACCATGGCTGC  
CTCCGAGCGCCGCGCTTCGCGCACAGATCAACAGGTAGTGTGGCCGCGGGG  
 CCCCCTCCACCTCCC

Exon 72530 to 72670

CCAATGGCCCCCTCCCTATCTTTCCAGGACGGTGGCCGCAGAGGTGCGGAAG  
CAGGTGTCCCGGAACGCAGTGGCTCCCCCACTCCAGCAGGCGCTGCAGCA  
GCTCCCTGGGGGTAAAGTATTTGGGGGTCCGCCCCCA

Exon 73300 to 73530

TCACAGCCACTTTGCTCCAATCCAGGTCCCACTGACTGAAGTTGTGAGCCCC  
TGGACTTTGAGGATGTACTTCTGAGCCGGCCACCAGATGCTGAGCCCGGGCC  
CCTCAGGGACCTGGTAGAATTCCCAGCTGATGACTTGGAGCTGCTGCTGCAG  
CCCCGGGAATGCCGACCACGGAGCCCGGGATCCCCAAGGATGAGTGGGTTC  
 AGCCCCACGCCCTCTCTGCCTG

Exon 73700 to 73830

GTCTCTGTTTACCCTGATCTTCTTTTGCTGCAGAAACTGGATGCCCAGGTGA  
GGCCGCGGTGGAGATGTATATTGAGGACTGGGTCATTGTCCACAGAAGGTG  
 AGTCTGACTTAGGGGCAGCTCAGGGG

Exon 74010 to 74190

CCTGCCAGCCCCGTTTCTGCTAGGTATCAGTACCTGAGTGCAGCATACAGC  
CCCGTCACCACAGACACACAGCGGGAGCGACAGAAGGGCCTCCCCCGCCAG  
GTCTTTGAGCAGGATGCTTCTGGAGACGAGAGGTCCGGCCCTGAGGACTCGG  
 TGAGGAAGCCCCCTGGCTGGGGTCAC

Exon 75170 to 75450

CAGTGCTTGACATTCTCCACTGGCAGAATGACTCCCGGCGTGGCTCGGGCTC  
CCCGGAAGACACCCCTCGAAGCAGTGGTGCCTCTAGCATCTTCGACCTGAGG  
AACCTGGCAGCTGACTCATTGCTGCCCTCTCTGCTAGAGCGGGCGGCCCCAG  
AAGATGTGGACCGGCGCAATGAAACCTTCGACGGCAGCACCGGCCCCCGGC  
CCTGCTACCCCTCTACCGGCACCTGACGAGGTGGGTGCCCTTCCAGATAT  
 CAGCCAACCAAGCATTTACT

FIG. 6A (1 of 7)

Exon 78100 to 78250

CCCGCCCAGCTCCACCCCCCACTCTTGGCAGGATGAAGCCGTGGAACGCTG  
TAGCCGCCCAGAGCCACCCCGCAGCACTTTGGACAAAGGATCTTGGTCAAG  
TGTCTGTCGCTCAAGTGAGTATACTGACATGTCTCTCTTCTTAGATG

Exon 80380 to 80500

CCCCCTCCCTCCCATTTACTTGTAGGTTGAGATTGAAATTGAGCCCATCTTT  
GGGATCTTGGCTCTGTATGATGTGCGGGAGAAAAAGAAGGTAGGAGGCCCTT  
TTTTCTCTTTCCTCCC

Exon 80540 to 80750

GTGGTGGCCCAGCTGCCTCTGGTGTCCCCAGATCTCGGAGAACTTCTACTTCG  
ACCTGAACTCGGACTCCATGAAGGGGCTGCTTCGGGCTCATGGCACTGCCATCTCCACC  
CTGGCCCCGCTCTGCCATCTTCTCTGTGACCTACCCCTCACC  
TGACATCTTCTGGTCATCAAGGTGCCTGCTGGGGCTGGGCAAGGGGGTGGT

Exon 82370 to 82510

GCCTCACTGGATTTCATTCATCTGCCCCGCAGTTGGAGAAGGTGCTTCAGCAAG  
GGGACATCAGTGAGTGCTGTGAGCCTTACATGGTGTTGAAAGAAGTGGACAC  
AGCCAAGGTAAGCGTGTGGAGGCTGGACTAGGGGCA

Exon 82540 to 82760

GCTGAGCTGGCAGGGGACGGGGTCTCCCCACAGAACAAAGAGAAGCTAGAG  
AAGCTGCGCCTGGCGGGCCGAGCAGTTCTGCACCCGCCTGGGGCCGCTACCGCA  
TGCCCTTCGCCTGGACGGCCGTGCACTTGGCCAACATCGTGAGCAGCGCTGG  
GCAGCTGGACCGGGACTCTGACTCGGAGGGCGGTGAGGAGGCGGGGCTAAC  
AGGCTTGGGGCGGGG

Exon 82860 to 83060

CTTGGTCCCCCTTTTGTCAATTGTCATTCCCTCCCCTAGAGCGCCGGCCAGCCT  
GGACAGACCGCCGCGTCGCGGGGCCCCAGGACCGGGCGAGTAGTGGGGACGACG  
CCTGCAGCTTCTCTGGCTTCCGTCCAGCCACGCTAACTGTCACAAACTTC  
TTTAAGCAGGTGTCCTACCCTGGGGCCAGGGACTCTCCCACTCC

Exon 83100 to 83260

GCCCAGGCTGACGGGAGTGGGTCCCATGTAGGAGGCTGAGCGACTCAGTGAC  
GAGGACCTCTTCAAGTTCCTGGCTGACATGAGGCGCCCGTCGTCCCTGCTGCG  
GCGACTACGTCCCTGTGACTGGTGCGTGGCACACCCCATACACAAGAAGTATC  
ACTC

FIG. 6A (2 of 7)

Exon 84050 to 84270

GTGCAAACCGGTTCTTCCCTTCCCAGCCCAGCTCAAGATCGACATTTCTCCGG  
CTCCTGAAAATCCCCACTTCTGCCTCTCCCCTGAGCTGCTTCATATCAAGCCC  
TACCCGGACCCCAGGGGCCGGCCACCAAGGAGATTCTGGAGTTCCCCGCCC  
GCGAAGTCTATGCCCCCATACCAGCTACAGGTACGGCCTCTGGGGCCAGC  
TGGGCACTTGA

Exon 87940 to 88130

GCCCCGTGCCCTCTGACACCCCCATCCTGCCCCCACAGGAACCTGCTGTACG  
TGTACCCGCACAGCCTCAACTTCAGCAGCCGCCAGGGCTCCGTGCGCAACCT  
TGCTGTGCGAGTGCAGTACATGACAGGCGAGGACCCAGCCAGGCTCTGCCG  
GTCAGTGGCTGTGCCCCAGGGAAGGGGGGTAGGG

Exon 88140 to 88270

TGGGTCCCTCATGAATCCACTCTCCCAGGTCATCTTTGGCAAGTCCAGCTGCA  
GTGAATTTACCCGCGAGGCCTTCACACCGGTGGTCTACCATAACAAGTATGT  
AGGGGGACACGTGAGGAACCTTGGGGG

Exon 88470 to 88680

GCCCCAGCAGATCCCCCAGCCCGATTCTGCCAGGTCCCCGAGTTCTACGA  
GGAGTTCAAGCTGCATCTTCCAGCCTGCGTGACAGAGAACCATCACCTGCTG  
TTACCTTTCTACCATGTCAGCTGCCAGCCCCGGCCGGGCACTGCCCTGGAGAC  
ACCCGTGGGCTTTACTGTGAGCCGTCCCCCTCCCTCCCTCCCCCTGAGCCCTCC  
T

Exon 88680 to 88870

TCGTCCCCCAACCTGGCCGCAGACCTGACCTCCAGCCTCTCCCCAGTGGATCC  
CACTGCTGCAGCACGGGCGCTGAGGACCGGCCCTTCTGTCTCCAGTGTCT  
GTGGACCAGCCGCCGCCAGCTATTCCGTGCTCACACCCGATGTATGTGCCCT  
GGAGCTCCTGCCTGCCAATGCACTGTCCCCAG

Exon 89360 to 89530

CAGGGAGGGCTGACCAGTGCCACCTGGTGCCTCCCTCCCACAGGTGGCGCT  
TCCGGGCATGCGCTGGGTGGACGGTCACAAGGGCGTGTTCAGTGTGGAGCTC  
ACAGCCGTGTCTCTGTGCACCCCCAGGTACGGGTGGGCCGGGAACCAAGA  
GTCCCGCCCTGCTCC

Exon 89660 to 89980

TTCATTCCCTGAGGCCCCACCCTGCTCACTCCACATCCCTACCCAGGACCCCT  
ACCTGGACAAATTCTTCACCCTGGTGCACGTCCTGGAGGAGGGAGCCTTCCC  
ATTCCGGCTCAAGGACACTGTGCTGAGCGAGGGCAACGTGGAGCAGGAGCTG  
CGGGCCAGTCTTGCAGCACTGCGCCTGGCCAGCCCCGAACCCCTTGTGGCCTT  
CTCCCACCACGTGCTGGACAAGCTCGTGCGTCTGGTCATCAGGCCCCCGATC  
ATCAGTGGCCAGATTGGTAAGCGAATGTGGCCTCAGACCTCAGTTTCCCCATC  
CACATG

Exon 90480 to 90730

AGAGGCCTTGGGGCCTGGAACCTTGACCTCTGCTCTGCCCTGCAGTGAACCTG  
GGCCGTGGAGCCTTTGAAGCAATGGCCCATGTAGTCAGCCTTGTTACCCGGA  
GCCTGGAGGCAGCCAGGATGCCCGCGGTCACTGCCACAGCTGGCTGCCTA  
CGTCCACTACGCCTTTTCGCCTTCCTGGCACTGAGCCAGCCTCCCGGATGGTG  
AGTTTGTAGAAATCCCTGTGAGACGAGAAATATCTGGGAGAA

Exon 92870 to 93120

ATCACATCAGGTGGGTGGGTGGTTGACCCTATTCACTCCATCCTCAGGGGCCCC  
TCCAGTGACAGTGACAGGCTGCCACACTGGCCCGTGGCTCTGGTCGCCCCGC  
AAGCCTCTACCTGGCGCGTTCCAAGAGCATCAGCAGCAGCAACCCTGACCTC  
GCCGTGGCCCTTGCTCTGTGGATGACGAGGTTTCCCGCATCCTGGCCAGCA  
AGGTAGGGCAACGGGGGCCCTGGAATCTCCAGCCTCAGTGGT

Exon 97210 to 97390

GGCACCTCGCACTCTGTGACCCCTGCCTCTGTCCCCAGCTGCTTCACGAGGAG  
CTGGCTCTGCAGTGGGTGGTCAGCAGCAGTGCCGTACGCGAGGCCATCCTCC  
AGCACGCCTGGTTCTTCTTCCAGCTCATGGTGAGACCCCTCCTCCCTGCCTG  
GTGGCAAGAGACCCCACTGGAG

Exon 98770 to 98990

CAAATCCCACCCACAGCCCTCTCACCCACCCCAAGGTGAAGAGTATGGCGC  
TGCACCTGCTGCTTGGCCAGCGACTAGACACACCCCGCAAGCTGCGCTTCCC  
CGGACGCTTCTGGACGACATCACTGCCTTGGTGGGCTCTGTGGGCTGGAG  
GTCATCACCCGTGTCCACAAGGTGAGAGATGCAGGGTCTCAATGTGGGAAGA  
AACCTGAGGGAGG

Exon 103130 to 103340

GGGGCTGAGGTTTGGGTGTGTGGGTTGACAGGCACCTGTGTCCCCAGGATGT  
GGAGCTGGCCGAGCACCTCAACGCCAGCCTGGCTTTCTTCTCAGTGACCTTC  
TGTCCCTGGTGGACCGGGGCTTTGTCTTCAGCCTGGTCCGGGCCCCACTACAAG  
CAGGTAGGAGTGGGCGTGGGCAGGGTGGGCATGGCATGGATGGAAGGCGGA  
GC

FIG. 6A (4 of 7)



Exon 103340 to 103590

CAATGTTGACATCACTGATGGCCACCCCTCTCCTGCAGGTGGCCACGCGGCT  
CCAGTCGTCCCCTAATCCAGCAGCCCTGCTGACCCCTGCGCATGGAATTCACCCG  
CATCCTGTGCAGCCACGAGCACTACGTGACCCCTCAACCTCCCCTGCTGCCCCC  
TGTCACCTCCAGCCTCGCCCTCCCCCTCTGTGTCTCCACCACCTCCCAGGTG  
GGCTGCCTTCACTTCTGCCTCCTCTCTTTGACCTACAAC

Exon 103990 to 104220

TGACCCCTTGACCGCTGGCATCCCCATTTTTCCCCACTCTGCAGAGCTCCAC  
CTTCTCCAGCCAAGCCCCGGACCCCAAGGTGACCAGCATGTTCGAACTGAGT  
GGACCATTCGCGCAGCAGCACTTCCTAGCTGGGCTCCTGCTGACGGAGCTGG  
CACTGGCCCTCGAACCTGAGGCTGAAGGGTGAGCAGAGCTCCTGTCTAGCCCC  
AGGACAGGTGGGACAGTCCAG

Exon 104220 to 104480

GGAGCCATGTCCACCCTGTCCTGAGCACCTCATTACCCCATAGGGCATTCCTG  
TTGCACAAGAAGGCCATCAGTGCTGTGCACAGCCTGCTATGTGGCCATGACA  
CTGACCCCGCTACGCCGAGGCCACTGTGAAGGCTCGTGTGGCCGAGCTGTA  
CCTGCCACTGCTATCGATTGCACGGGATACCTTGCCACGGCTGCATGACTTTG  
CTGGTCAGTGGGCCAGGGGAAGATGGGGTCACATGATCCAGGGACTTGGTG

Exon 108850 to 109100

ACCAAGGGTTTATCTTTCTTTCCCTCTGTCTTTCCCTGCCAGAGGGCCCAGGTC  
AGCGGTCAAGACTGGCCTCAATGCTTGACTCAGACACAGAAGGCGAAGGGG  
ACATTGCGGGTACCATCAACCCCTCTGTGGCCATGGCCATTGCTGGTGGCCCCC  
TAGCCCCTGGCTCCCGGGCCAGCATCTCCAGGGGCCACCAACGGTGAGTA  
GGGAGGCTTGTCCTCATAGACATCATCCACTTTGAATGAGA

Exon 109140 to 109410

TCACATGGAGAAAATGGAAATTGACTTTGATTCTCTCTGGCCCCAGGCTTCT  
CGCGCAGGCTGTGCCCTCTCTGCTGAGTCAAGCCGGACCTTGCTGGCGTGTGT  
GCTGTGGGTGCTGAAAAACCCGAGCCGGCGCTCCTGCAGCGCTGGGCCACT  
GACCTGACACTCCCCCAGCTGGGACGTCTGTTGGATTGCTGTACCTTTGCCT  
AGCTGCCTTTGAGTACAAGGTTTGAGGGCGTGGGCAGGAGATGATGGAGGAG  
GCAGGCTA

Exon 110310 to 110530

GAAAAGAGCAGAGTCAGCCTGGAACCCAGTTCTCTGCACCCCAAGGGGAA  
AAAGGCCCTTTGAACGCATCAACAGCCTCACATTCAAAAAATCTCTGGATATG  
AAGGCGCGGCTAGAGGAAGCCATTCTGGGTACCATCGGAGCTCGACAAGAA  
ATGGTTCGGCGAAGTCGTGCTAAGAGGGTGACATACCCACGTGTCCCCATCC  
CACCAGCTGCTCCCA

Exon 110770 to 110940

TGTGTTTTTACGCATCTGTGATCGTGCACCCACGCGTCTCAGAGAGGAGCCCG  
TTTGGGAATCCGGAGAATGTGCGCTGGCGGAAGAGCGTCACACACTGGAAGC  
AAACCTCAGACCGCGTGGACAAGTAGGTGTGGGCAGGAGGGTGTCTGCTGAG  
TTCAGAACAGTTTG

Exon 111590 to 111770

ATCTCACCCCGAGTGGGCCCCCAAGACCTCCTTTCCCTTCCAGGACCAAGG  
ATGAAATGGAACACGAGGCCCTTGGTGGGAAGGGAACCTGGCAACCGAGGCAA  
GCCTAGTGGTTCTGGACACACTGGAGATCATCGTGCAGGTAGGGCTTGATCC  
AGCATCTGCCTTGTGCTCTGAGCCCA

Exon 111830 to 112050

ACCCTAGGCTCTAACACCTGGATTCTTGACCCCTTCCCTCCAGACGGTGATG  
CTTTCAGAAGCCCGGGAGAGCGTCTTGGGGGCAGTGCTGAAGGTTGTGCTGT  
ACAGCCTGGGCAGTGCCCAGAGTGCCCTCTTCTTGACGATGGCCTGGCCAC  
CCAGAGGGCCCTTGTGTCCAAGGTGAGCACCCTCAACAACCATGATTCTTA  
GAAAAACAGTAG

Exon 112910 to 113140

AACGGGGAGGGGCTGGACAGTGTCTGTCTGGGTCCCTGGGGGCAGTTCCCGG  
AGCTGCTGTTTCGAGGAGGACACGGAGCTGTGTGCCGACCTGTGCCTGAGGCT  
CCTACGACACTGTGGCAGCCGCATCAGCACCATCCGCACGCACGCCAGCGCC  
TCGCTGTACCTGCTCATGCGACAGAACTTCGAGATCGGCCACGTGAGTGGGG  
GCTAGGAGGCATGGTCCACACATGGCTCTGGTC

Exon 114090 to 114340

TCTGAGACTCCCGGCTCCACCCTCCCGCCCCTGTCCCTGCAGAACTTTGCCCC  
TGTGAAGATGCAGGTCACCATGTCTCTCTCGTCCCTGGTGGGGACGACGCAG  
AACTTCAGTGAAGAGCACCTGCGACGTTCACTCAAAACCATCCTCACCTATG  
CTGAGGAGGACATGGGGCTGCGGGACAGCACCTTCGCAGAGCAGGTGACAC  
CTGCTGGGTCCCCGCCCCGCTCCCTTCATATAACTCCCAAC

FIG. 6A (6 of 7)

Exon 114370 to 114550

ATGCTCTCATTGGCCCCCTGGACGTTCCCCGGCTCCAGGTCCAGGACCTGATGT  
TCAACCTGCACATGATCCTGACGGACACGGTGAAGATGAAGGAACACCAGG  
AGGACCTGAGATGCTCATCGACCTCATGTACAGGTGAGGTGGGCCAGCTGG  
CACCTTCAGCCACGCCCACGCCCA

Exon 116900 to 117170

AGGTGAGTCCCCTCCTCACATCCCCCTCACCTGGACTCCAGAATTGCCCGGG  
GCTACCAGGGCTCACCGGACCTTCGGCTGACCTGGTTGCAGAACATGGCCGG  
GAAGCACGCGGACGTGGGCAACCACGCCCAGGCCGCCAGTGCATGGTGCA  
CGCGGCCGCCCTCGTGGCTGAGTACCTCGCCCTGCTCGAGGACCAGCGCCAC  
CTGCCCCGTGGCTGGCGATTTCCTTCCAGGTGAGTGGCCAGGGGTGGCAGGT  
GGCGGACGGCA

Exon 117170 to 117410

ACGAGTGCAGTGGGGACCAGGGTCTGACGCCACCTCTCCCACCCAGAACAT  
CTCATCCAACGTGCTAGAGGAGTCCGCCATCTCCGACGACATCCTGTGCCCC  
GACGAGGAGGGCTTCTGCTCCGGGAAGCACTTCACTGAGCTGGGGCTGGTAG  
GGTTGCTGGAACAGGCAGCCGGCTACTTCACCATGGTGAGGCCTTGGGGACT  
GGGTGCAGGAGAGGGGGCTCGGGCCAGGGAGGT

Exon 121670 to 121900

GAGAGGAAGACAGTTTGGGGAATCCTGACCCACCTCACCCCTCAGGGCGGGC  
TCTACGAGGCGGTGAATGAGGTCTACAAGAACCTCATCCCCATCCTGGAAGC  
CCACCGTGACTACAAGAAGCTGGCCGCGGTGCACGGCAAACCTGCAGGAGGC  
CTTACCAAGATCATGCACCAGGTGGGCCCAGGACCCCTCCCCAGACCCCA  
CCCTCAGCCCCACTCCTCATCC

Exon 121910 to 122000

CCCCAGGGATCTGCTGACCTTGACCCTTCTCTTCCCCACAGAGTTCGGGTGG  
GAGGTGAGTCAGCCTTGGTGGACAGCCACCTGCCTCTG

Exon 123290 to 123510

TCCAGCAGGGGCCTCCCGGACAACCACACCCTTTCTCACAGCCCCAGCGCGT  
GTTCCGGACGTATTTCCGCGTGGGCTTCTACGGCGCCCACTTCGGTGACCTGG  
ATGAGCAGGAGTTTGTGTACAAGGAGCCATCGATCACGAAGCTGGCAGAGAT  
CTCACACCGGCTGGAGGCATGTCCTTGTGTTGGGGGTGGAACGGGGCATGG  
GGCTGCCTTGGG

Exon 123510 to 123633 (end clone)

GGCTGGAGTAGGGGCTGTCCCTGGGTGGCCCCGAGTCAGCCCTGTGTCTCCA  
GGAGTTCTACACGGAGAGATTGGCGACGACGTCGTTGAGATTATCAAAGAC  
TCTAACCTGTGGACAAGTC

FIG. 6A (7 of 7)

GGGCATGTGGCTCATTCTGTAATCCCGGCACTTTGGGAGGCGGAGGCGGGTGGATC  
 ACCTGAGGTCAGGAGCTCCAGACCAGCCTGGCCAACATGGTGAAACCCCGTCTCTAC  
 TAAAAATACAAAAAATTAGCCAGGTGTGATGGTGGGTGCCTGTAATCCCAGCTACTC  
 GGGAGGGCTGAGGCAGGAGAATCGCTTGAACCTGGGAGGCAGAGGTTGCGGTGAGCC  
 GAGATTGTGCCATTGCACTCCAGTCTGGGCAACAAGAGCGAAATGCCACCTCAAAAT  
 AAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAGAGGATAA  
 AATGCCAGCAACCCATAGATGGGAATGAGAACAGCACGTGCAAAGGCCCTGAGGCA  
 GAGCCACGGCCTTGTCTGATTCAACCTCAAATTCTCCCTGGGGCATTGTGCTGACCAGG  
 GAAAGAAGGGCTGTCCAGGAGGAAGGACCTGCCGGTGCAGAGGCATGCAGGTGAGA  
 AAGGGGTGAGCTCCTCCAGAGGGGAGTGTGGCTGGGAGAATTCTCTAAAAATGCTGC  
 AGCAGTGTGGGAGAGAGGCCAGTGGGGAGAGATTTGAGACCATAGATTAACCAAG  
 ACATCCCCACCTCTTCTCTTGGTAGAGGCGGCCCGAAAGTCTAGACTCCCAAACT  
 GGCTCACTCAGGTCCCACCCTGGACCTGGGGCACATCTCCGAGCACTCCAGTGCC  
 TAGCCAGGCTCCTCTGACTCCCATGCTGTAGACTGGGAGCACGGACAATGCAGGCGC  
 TGGAGACCCCTGTGAGTCACACTGAGCAAGCACCCGAACACCTCTGTGCCTCAGTTT  
 ACTCATCTGTAAAAGGAGGAAAACAATAATTTCTTCTGCATGTGTGAATTGCAGGGC  
 CAGGCTCAATGACATCTTAGCAATTAGACTTTTTGAGACAGGGTCTCGCTCTGTACC  
 CAGGCTGGATTGAAATGGCACAATCACAGCTCACTGCAGCCTTGACCTCCCAGGCTC  
 AAGCGATCCTCCTCCTCAGACTCCCAAGTAGCTGAGATTACAGGCACACACCACCA  
 TGCCTGGTTAATTTTGCATTTTTTGTGGACACGGGGTCTCATTATGTTGCCAGGCT  
 GGTCTCCAACCTCCTGGGCTCAAACAATCCTCCTGCCTTGGCCCCCAGTGTGTTGGG  
 ATTACAGGCATGAGCCACCATGCACGGCCACGATTATACTTACAGGTATGATTATTA  
 GATACATGAACATCGTTATTGTTTTCCAGCCAGGAGTCAGAGGGCAGAAAGAGCGCC  
 CCCCAGAGCCCGGAAATCTGGGGCCTACCCAGCCTGGGTCCCAGCGCCTCCCTCCC  
 TCCCTCCTCCTGAGCTTCAGTTTCCCCAGCCCTGCTCCTGGGGTGGTAAGACCACCC  
 CACTAAACCCCGGAGCCTGGGGTCCACCTAGCCCGGGTCTCAGCGCCTCCCTCCC  
 TCCCTCCCTCCTCAGGCTCAGTTTCTCCAGCCAGCTCCAGGGTGAAAGAGCGCC  
 CCCGCCAGCTCGGGAGTCTGGGGCACCCCAAGTCTGGGTCCCAGCGCCTCCTCTCCC  
 TAACTTCCCTCCTCAGCCTCAGTTTCCCCAGCCCTTCTCCTAGGGTAGAAAGAGCGTC  
 CCCCCAGCCCGGGAGTCTGGGGCCCGCCAGCCTGGATCCCGGGGCTCCTCTCCGT  
 CCCCAGCCTCAGTTTCCCCAGCCCCAGGACTCCAGGCGACCCCTCCGGCTGCAGG  
 GGCAGCACGGAGCGGCCCGGGCCACCCGGAAGGGCCCCGCCCCGCGCCGCCCCG  
 CCCCCGCCCCGGCTGCCAGAACCGGGAGGCGGGCGGGCGGGCGGGGCCCCG  
 GGGCGGCGGGCGGGACGCGAGGACCATGGCTGCCTCCGAGCGCCGCGCCTTCGC  
GCACAAGATCAACAGG

FIG. 6B

```

hCLASP4 -----MFPMEDISISVIGRQRRTVQ----- 20
hCLASP5 -----MTHLNSLDVQLAQELG----- 16
hCLASP3 -----MAERRAFAQKISRTVAAEVRKQISGQYSGSPQLLKNLNI 41
hCLASP2 -----MLLFYDDFQTAILRRQGRYICS----- 23
hCLASP7 -----MAASERRAFAHKINRTVAAEVRKQVSRERSGSPHSSRRCSS 43
hCLASP1 MSFRGKVFKREPSEFWKKRRTVRRVIOEEFHRFSQEKPRLLEPLDYETVIEELEKTYRN 60
      . . .

hCLASP4 -----STVPEDA EKRAQSLFVKECIKTYSTDWHVVNYK 53
hCLASP5 -----DFT 19
hCLASP3 N-----ISHHTTVPLTEAVDPVDLEDYLI THPLAVDSGPLRDLIEFP 83
hCLASP2 -----TVPKAE EEAQSLFVTECIKTYNSDWHVLVNYK 55
hCLASP7 G-----VPLTEVVEPLDFEDVLLSRPPDAEPGLRDLVEFP 79
hCLASP1 DPLQDLLFFPSDDFSAATVSWDIRTYLSTVPEDA EHKAE NLLVKEACKFYSSQWHVVNYK 120
      : :

hCLASP4 YEDFSGDFRMLPCKSLRPEKIPNHVFEIDEDCEKDED-----SSSLCSQKGGVIKQG 105
hCLASP5 DDDL DVVFTPKECRTLQP-SLPEEGVELDPHVR-----DCVQTYIREWLI 63
hCLASP3 PDDIEVVYSPRDCRTLVS-AVPEE-SEMDPHVR-----DCIRSYTEDWAI 126
hCLASP2 YEDYSGEFRQLPNKVVKLDKLPVHVVEVDEEVDKDED-----AASLGSQKGGITKHG 107
hCLASP7 ADDLELLLQPRECRTEP-GIPKD-EKLD AQVR-----AAVEMYIEDWVI 122
hCLASP1 YEQYSGDIRQLPRAEYKPEKLP SHSFEIDHEDADKDED TTS HSSSKGGGAGGTGVFKSG 180
      : : . : * . : * .

hCLASP4 WLHKANVNSTIT--VTMKVF KRRYFYLTQLPDGSYILNSYKDEKNSKESK-GCIYLDACI 162
hCLASP5 VNRKNQGSPEIC--GFKKTGSRKDFHKT-LPKQTFESETLECSEPAQA--GPRHLNVLC 118
hCLASP3 VIRKYHKLGTGF--NPNTLDKQKERQKG-LPKQVFESDEAPDGN SYQDDQDDLKR RSM SI 183
hCLASP2 WLYKGNMNSAIS--VTMRSFKRRFFHLIQLGDGSYNLNFYKDEKISKEPK-GSIFLDSCM 164
hCLASP7 VHRRYQYLSAAY--SPVT TDTQ RERQKG-LPRQVFEQDASGDERSGPEDSND SRRGSGSP 179
hCLASP1 WLYKGNFNSTVNNTVTVRSFKKRYFQLTQLPDNSYIMNFYKDEKISKEPK-GCIFLD SCT 239
      : : . : : * : : . : .

hCLASP4 DVVQC PKMRRHAFELKMLDKYSHYLA AE TEQEME EWLITLKKIIQINTDSL VQEKKETVE 222
hCLASP5 DVSGKG PVTACDFDLRSLQPD KRLNLLQQVSAEDFEKQNEEARRTN-----RQAE 169
hCLASP3 DDTPRGSWACSI FDLKNSLPDALLPNLLDRTPNEEIDRQND DQRKSN-----RHKE 234
hCLASP2 GVVQNNKVRRAFELKMQDKSSYLLAADSEVEME EWITILNKILQLN-----FEAAMQEK 219
hCLASP7 EDTPRSSGASSI FDLRNLAADSL LPSLLERAAPEDVDRRNETLRRQH-----RPPA 230
hCLASP1 GVVQNNRLRKYAFELKMNDLTYFVLAETESDMDEWIHTLNRILQISPEGPLQGRRSTEL 299
      * : : . : :

hCLASP4 TAQDDETSS---QGKAENIMASLERSMHP ELMKYGRETEQLNKLSRGDGRQNLFSFDSE 278
hCLASP5 LFALYPSVD---EEDAVEIRPVPEC PK EHLG-----N-----RILVKLLTLKFEIE 212
hCLASP3 LFALHPSPD---EEEP IERLSVPDIPKEHFG-----QRLLVKCLSLKFEIE 277
hCLASP2 RNGDSHEDD---EQSKLEGSGSGLSYLP ELAKSAREAEIK---LKESERVKLFYLDPD 272
hCLASP7 LLTLYPAPD---EDEAVERCSRPEPPREHFG-----QRLVKCLSLKFEIE 273
hCLASP1 TDLGLDSLNSVTCECTPEETDSS ENNLHADFAKYLTETEDTVKTTNRMERLNLFSLDPD 359
      . : : : : : : : : : :

hCLASP4 VQRLDFS---GIEPDIKP-FEECKNKRFLVNCHDLTFN ILGQIGDNAKG PPTNVEPFFI 333
hCLASP5 IEPLFAS---IALYDVKERKKISENFHCDLNSDQFKGFLRAHTPSVAASSQARS AVFSV 268
hCLASP3 IEPIFAS---LALYDVKEKKKISENFYFDLNSEQMKGLLRPHVPPAAITTLARSAIFSI 333
hCLASP2 AQKLDFS---SAEPEVKS-FEEKFGKRILVKCNDSL FNLQCCVAENE EGPTTNVEPFFV 327
hCLASP7 IEPIFGI---LALYDVREKKKISENFYFDLNSDSMKGLLRAGHTHPAISTLARSAIFSV 329
hCLASP1 IDTLKLQKKDLLEPESVIKPFEEKAAKRIMIICKALNSNLQGCVTENENDPITNIEPFFV 419
      : : . : : . : : : : : * :

```

FIG. 7 (1 of 6)



	FKSHLESTIYTYQDLHVHKFFHHQCQLIQS-----GSKEVPGGELIKYLKCLHAM	794	
hCLASP4	IEVQAVSSVHTQDNHLEKFFTLCBSLESQVTFPPIRVLDQKISEMALEHELKLSIIICLNSS	715	
hCLASP5	VEVVAVSSIHTQDPYLDKFFALVNALDEH-LFPVRIGDMRIMENNLENLKSSISALNSS	780	
hCLASP3	ISTHLVSTVYTQDQHLHNFFQYCQKTES-----GAQALGNELVKYLKSLHAM	787	
hCLASP2	VELTAVSSVHPQDPYLDKFFTTLVHVLEE--AFPFRLKDTVLSEGNVEQLERASLAALRLA	767	
hCLASP7	VSTFVVSTVNTQDPHVNAFFQECCQREKD-----MSQSPTS NFIRSCKNLLNVE	887	
hCLASP1	..       *: :.* ::. ** : :.	:	*
<hr/>			
hCLASP4	EIDVMIOQLFLPVILMQLEF-----VLTNMTH-----EDDVP	824	
hCLASP5	RIEPLVLFLHLVLVDKLFQLSVQPMVIAGQTANFSQFAFESVVAIANSLHNSKDLSKDQH	775	
hCLASP3	QLEPVRVRFLLHLLDKLILLLVIRPPVIAGQIVNLGQASFEAMASIINRLHKNLEGNDHQH	840	
hCLASP2	EGHVMIAFLPTILNQLEF-----VLT-RAT-----QEEVA	816	
hCLASP7	SPEPLVAFSHHVLDKLVRLVIRPPIISGQIVNLGRGA FEAMAHVSVSLVHRSLEAAQDARG	827	
hCLASP1	KIHAIMSF LPI ILNQLEF-----VLVQNE-----EDEIT	916	
	. : : * : * : *	:	::
<hr/>			
hCLASP4	INCTMV-LLHIVSKCHEEGLDS-----YLR SFIKYS-----FRPEKP	860	
hCLASP5	RNCLLAS YVHYV FRLPEVQRDVPSKGAPTALLDPRS YHTYGR TSAAAVSSKLLQARVMSS	835	
hCLASP3	RNSLLASY IHYV FRLPN TY PNSSSPG-PGGLGGSVHYATMARSA VRPASLNLNRSRSLSN	899	
hCLASP2	VNVTRV-IIHVVAQCHEEGLES-----HLRSYVKYA-----YKAEPY	852	
hCLASP7	HCPQLAAYVHYAFRLPGTEPSLPDGAPP---VTVQAATLARGSGRPASLYLARSKS ISS	883	
hCLASP1	TTVTRV-LPDIVAKCHEEQ LDH-----SVQSY IKFV-----FKTRAC	952	
	.	:	:
<hr/>			
hCLASP4	SAPQAQLIH-----ETLAT TMIA I LKQS-----	883	
hCLASP5	SNPDLAGTHSAADEEVKNIMSSKIADRNC SRMSYYCSGSSDAPSSPA-----	882	
hCLASP3	SNPDISGTPTSPDDEVRSIIGSKGLDRSNSWVNTGGPKAAPWG SNSPSPAESTQAMDRSC	959	
hCLASP2	VASEYKTVH-----EELTKSM TILKPS-----	875	
hCLASP7	SNPDLAVAPGSVDDEVSRILASKLLHEELA-LQ-----	915	
hCLASP1	KE---RPVH-----EDLAKNVTGLKSN-----	972	
	:	:	:
<hr/>			
hCLASP4	-----ADFLSINKLLKYS-----WFFFEI I AKSM	907	
hCLASP5	-----APRPASKKH FHEELALQ-----M VVSTGMVKSM	910	
hCLASP3	NRMSSH TETSS FLQTLTGRLPTKKLFHEELAQ WVVC SG SVRESALQQAWFFFEL MVKSM	1019	
hCLASP2	-----ADFLT SNKLL RYS-----WFFFDVLIKSM	899	
hCLASP7	-----WVVSS SAVREAILQHA-----WFF FQLMVKSM	942	
hCLASP1	-----DSPTVKHVLKHS-----WFFFA I ILKSM	995	
	.	*	: ***
<hr/>			
Cadherin Cleavage			
hCLASP4	ATYLEENKIKLERGORFPETYHVLHSLLLAIIPHVTIRYAEIPDE---SRNVNYSLAS	964	
hCLASP5	AQHVNMDKRDSERRTRFS DRFMDDITTIVNVVTSEIAALLVKPQKENEA QAEKMNISLAF	970	
hCLASP3	VHHLYFNDKLEAFRKSRFPERFMDDIAALVSTIASDIVSRFQK DTEM---VERLNTSLAF	1076	
hCLASP2	AQH LIENS KVKLI RNQRF PAS YHHAAETVV NMLMP HITQKF GDNPEA---SKNANHSLAV	956	
hCLASP7	ALHLLLQGRLDTERKLRFPGFRFLDDITALVGSVGLEVITRV HKDVEL---AEHLNASLAF	999	
hCLASP1	AQHLLDTNKIQLHRPQRFPE SYQNELDNLMVLS DHVITWKYKDALEE---TRRATHSVAR	1052	
	. : : . : * * * . : : . : . : . : . : *	:	:
<hr/>			
hCLASP4	FLKRCLTLMDRGFIFNLINDYISGFSPKDP----KVL AEYKFEFLQ TICNHEHYI PLNL	1019	
hCLASP5	FLYDLLSLMDRGVFENLIRHYCSQLSAKLSNL---FT LISMRLEFLRILCSHEHYLN LN	1027	
hCLASP3	FLNDLLSVMDRGVFVFLSIKSCYQVSSKLYSLPNPSVLVSLRLDFLR IICSHEHYVT LNL	1136	
hCLASP2	FIKRCFTFMDRGVFVKQINNI ISCFAPGD P----KTLFEYKFEFLRVVCNHEHYI PLNL	1011	
hCLASP7	FLSDLLSLVDRGVFVSLVRAHYKQVATR LQSSPNPA ALLTLRMEFTRI LCSHEHYVT LNL	1059	
hCLASP1	FLKRCFTFMDRGVFCVMNNYISMFS SGD L----KTL CQYKDFLQEVQCQEHFIPLCL	1107	
	* : : : : * * * : * . : . : . : . : . : * * * : *	:	:

FIG. 7 (3 of 6)

Cadherin EC motif

hCLASP4	PMAFAKPKLQR-----VQDS--NLEYSLSDEYCKHHFLVGILLRETSI	1060
hCLASP5	FFMNADTAPTSP--CPSISSQNSSSCSSSFQDQKIASMFDLTSEYRQQHFLTGLIFTELA	1085
hCLASP3	PCSLLTTPASPSPSVSSATSQSSGFTSNVQDQKIANMFELSVFPRQQHYLAGIVLTELA	1196
hCLASP2	PMPFGKGRIQR-----YQDL--QLDYSLTDEFERNHFLVGILLREVGT	1052
hCLASP7	PCCPLSPASPSPSVSSTTSQSSTFSQAPDPKVTSMFELSGPFPRQQHFLAGILLTELA	1119
hCLASP1	PIRSANIPDPLTP-----SES----TQELHASDMPEYSVTNEFCRKHFLIGILLREVGF	1157
	. : : : : : * : : : *	
hCLASP4	ALQDN----YETRYTAISVIKNNLLIKHAFDTRYQHKNQAKIAQLYLPFVGLLENIRL	1116
hCLASP5	ALDAEGEGISKVQRKAVSAIHSLLSSHDLDPRCVKPEVKVIAALYLPVGIILDALP--	1143
hCLASP3	ILDPDAEGLFGLHKKVINMVHNNLLSSHSDSDPRYSDPQIKARVAMLYLPLIGIIMETV--	1254
hCLASP2	ALQEFR----EVRLLIAISVLKNNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVORI	1108
hCLASP7	ALEPEAEGAFILHKKAISAVHSLLCGHDTDPRYAEATVKARVAELYLPLLSIARDTLP--	1177
hCLASP1	ALQEDQ----DVRHLALAVLKNLMAKHSFDDRYREPRKQAQIASLYMPLYGMLLDNMPRI	1213
	* : : : : : * * * : : : * * : : *	
hCLASP4	AGRDTLYSCA-----AMPN-S----ASRDEFPCGFTSPANRGSLSLTDKDTAYGS	1160
hCLASP5	-----QL-----CDFTVADTRRYRTSGSD----	1162
hCLASP3	-----QLY-----DFTETHNQGRGPCIATDD--	1276
hCLASP2	NVRDVSPFPVNAAGMTVKDESLALPA-VNPLVTPQKGSTLDNSLHKDLLGAISGIASPYTT	1167
hCLASP7	-----RLH-----DFAEGPGQSRSLASMLSDTE	1201
hCLASP1	YLKDLYPFTVNTSNQGSRDDSLSTNGGFQSQTAIKHANSVDTSFSKDVLSNIAAFSSIAIS	1273
	. : .	
hCLASP4	FQ-NGHGIKREDSRGS LIPEGATGFPDQNGTGEN-----TRQSSTRSSVSQYNRLDQYE	1213
hCLASP5	-----EEQEGAGAINQNVALAIAGNNFNLT-----SGIVLSSLPYKQYNMLNADT	1208
hCLASP3	-----YESESGSMISQTVAMAIAGTSVPQLTR---PGSFLTSTSGRQHTTFAES	1324
hCLASP2	STPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDDKHQQSSTLGNSSVVRCDKLDQSE	1227
hCLASP7	-----GEGDIAGTINPSVAMAIAGGPLAPGSR---ASISQGPPTASRAGCALSAES	1249
hCLASP1	-----TVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRPLALIGSTLRFDRLDQAE	1327
	. : . : .	
hCLASP4	IRSLLMCYLYIVKMISEDTLLTYWNKVSPQELINILILLEVCLFHFYRMGKRNIARVHDA	1273
hCLASP5	TRNLMICFLWIMKNADQSLIRKWIADLPSTQLNRILDLLFICVLCFEYKGKQSSDRVSTQ	1268
hCLASP3	SRSLLICLLWVLKNADETVLQKWFDTLSVLQLNRLLDLYLCVSCFEYKGKQVFERMNSL	1384
hCLASP2	IKSLLMCFLYILKSMSDDALFTYWNKASTSELMDDFFTISEVCLHQFQYMGKRYIARNOEG	1287
hCLASP7	SRTLLACVLWVLKNTTEPALLQRWATDLTLPQLGRLLDLYLCLAAFEYKGKKAFAFEHINSL	1309
hCLASP1	TRSLLMCFLHIMKTISETLIAYWQRAPSPPEVSDFFSILDVCLQNFYRLGKRNIIRKIAA	1387
	. : * * : * . : : : : : * : * * : *	
hCLASP4	WLSKHFGIDR-----KSQTMPALNRNSGVQARLQHLSSLESS-----	1311
hCLASP5	VLQKSRDVKAR-----LEEALLRGEARGEMMRRRAPGNDRFPGLNEN---	1311
hCLASP3	TFKKSMDMRK-----LEEAILGSIGARQEMVRRSRGQLERSPSGSAFGSQ	1430
hCLASP2	LGPIVHDRKS-----QTLPVSRNRTGMMHARLQQLGSLDNS-----	1323
hCLASP7	TFKKSMDMKAR-----LEEAILGTIGARQEMVRRSRERSRSPFGNPEN----	1350
hCLASP1	AFKFVQSTQNNGTLKGSNPSCQTSGLLAQWMHSTSRHEGHKQHRSTLPIIRGKN----	1442
	. : .	
hCLASP4	-----FTLNHSSTTTEADIFHQALLEGNTATEVSLTVLDTISFETQCFKTQLL	1359
hCLASP5	--LRWKKEQTHWRQANEKLDKTKAELDQEALISGNLATEAHLIILDMQENIIQASS-ALD	1368
hCLASP3	ENLRWRKDMTHWRQNTTEKLDKSRAEIEHEALIDGNLATEANLIILDTLEIVQTVS-VTE	1489
hCLASP2	-----LTFNHSYGHSDADVHLQSLLEANIATEVCLTALDTLSLFTLAFKNQLL	1371
hCLASP7	--VRWRKSVTHWKQTSRDRVDKTKDEMEHEALVEGNLATEASLVVLDLTLIIVQTVM-LSE	1407
hCLASP1	--ALSNPKLLQMLDNTMTSNSNEIDIVHHVDTEANIATEGCLTILDVLSLFTQTHQRQLQ	1500
	. : : : . * * * * * * * .	

FIG. 7 (4 of 6)



hCLASP4 NNDGHNPLMKKVFDIHLAFLKNGQSEVSLKHVFASLRAFISKFPFAFFKGRVNMCAAFY 1419  
hCLASP5 CKDS---LLGGVLRVLVNSLNCDSSTYTLTHCFATLRALIAKFGDLLFEEVEQCDFDLCH 1425  
hCLASP3 SKES---ILGGVLKVLHSMACNQSAVYLQHCFAQRALVSKFPELLFEEETEQCADLCL 1546  
hCLASP2 ADHGHNPLMKKVFVDVYLCLQKHQSETALKNVFTALRSIYKFPSTFYEGRADMCAALCY 1431  
hCLASP7 ARES---VLGAVLKVVLYSLGSAQSALFLQHGLATQRALVSKFPELLFEEDTELCADLCL 1464  
hCLASP1 QCDCQNSLMKRGFDTYMLFFQVNSATALKHVFASLRFLVCKFPFAFFQGPADLCGSFCY 1560  
. : : : : \*\* \* : : : \* : : \*\* . : : \* : \*

hCLASP4 EVLKCCTSKISSSTRNEASALLYLLMRNFEYTKRKTFLRTHLQIIIAVSQLIADVALSGG 1479  
hCLASP5 QVLHHCSSSDVTRSQACATLYLLMR--FSFGATSNFARVVKMQVTMSLASLVGRAPDFNE 1483  
hCLASP3 RLLRHCCSSSIGTIRSHPSASLYLLMR--QNFEIGNNFARVVKMQVPMSLSSLVGTSQNFNE 1604  
hCLASP2 EILKCCNSKLSSIRTEASQLLYFLMRNFDYTGKKSFVRTHLQVIIISVQLIADVVGIGE 1491  
hCLASP7 RLLRHCGSRISTIRTHASASLYLLMR--QNFEIGHNFARVVKMQVTMSLSSLVGTQNFSE 1522  
hCLASP1 EVLKCCNHRSRSTQTEASALLYLFMRKNFEFNKQKSIVRSHLQLIKAVSqliADAG-IGG 1619  
.:\* : \* : : : : \*\* : : : : : : : : : : : : : : : .

hCLASP4 SRFQESLFIINNFA NSDRPMKATAFPAEVKDLTKRIRTVLMATAQMKEHEKDPEMLIDLQ 1539  
hCLASP5 EHLRRSLRTILAYSEEDTAMQMPPTQVEELCLNLSILYD TVKMEFQEDPEMLMDLM 1543  
hCLASP3 EFLRRSLKTIITYAEEDLELRETTFPDQVQDLVFNLMILSDTVKMEHQEDPEMLIDL 1664  
hCLASP2 TRFQQSLSIINNCANSRDLIKHTSFSSDVKDLTKRIRTVLMATAQMKEHENDPEMLVDLQ 1551  
hCLASP7 EHLRRSLKTIITYAEEDMGLRDSSTFAEQVQDLMFNLMILTDTVKMEHQEDPEMLIDL 1582  
hCLASP1 SRFQHS LAITNNFANGDKQMKNSNFAEVKDLTKRIRTVLMATAQMKEHEKDPEMLVDLQ 1679  
: : \*\* : : \* : : : \* . : : : : : : : : : : : : : : : \*

transmembrane  
hCLASP4 YSLAKSYASTPELRKTWLD SMAKIHVKNGLFSEAAMCYVHVAALVAEFLHRKK----- 1592  
hCLASP5 YRIAKSYQASPDRLRLTLQNM AEKHTKKKCYTEAMCLVHAAALVAEYLSMLEDH----- 1598  
hCLASP3 YRIAKGYQTSPE-RLTLQNMAGKHSERSNHAEAAQCLVHSAALVAEYLSMLEDR----- 1718  
hCLASP2 YSLAKSYASTPELRKTWLD SMARIHVKNGLDSEAAMCYVHVTALVAEYLTRKG----- 1604  
hCLASP7 YRIARGYQGPSDLRLTLQNMAGKHAELGNHAEAAQCMVHAAALVAEYLLALLEDQ----- 1637  
hCLASP1 YSLANSYASTPELRRTWLESMAKIHARNGLDSEAAMCYIHIAALIAEYLRKRGYWKVEKI 1739  
\* : \* . \* : : \* \* : : \* \* \* : : \* : : \* : : \* : : \*

hCLASP4 -----LFPNGCSAFKKITPNIDEEGAMKEDAGMMD---- 1622  
hCLASP5 -----SYLPVGSVSFQNISSNVLEESVVS EDTLSPDEDGV 1633  
hCLASP3 -----KYL PVGCVTFQNISSNVLEESAVSDDVSPDEEGI 1753  
hCLASP2 -----VFRQGCTAFRVITPNIDEEASMMEDVGMQD---- 1634  
hCLASP7 -----RHL PVGCVSFQNISSNVLEESAISDDILSPDEEGF 1672  
hCLASP1 CTASLLSE DTHPCDSNSLLTTPSGGSMFSGWPAFLSITPNIKEEGA AKEDSGMHD---- 1795  
: \* : \* \* : : \* : : \* : \*

ITAM  
hCLASP4 ---VHYSEEV LLELLEQCVDGLWKAERYEIISEISKLIVPIYEKRRFEKLTQVYRTIHG 1679  
hCLASP5 CAGQYFTESGLVGLLEQAAELFSTGGLYETVNEVYKLVIPILEAHREFRKLTTHSKLQR 1693  
hCLASP3 CSGKYFTESGLVGLLEQAAASFMSAGMYEAVNEVYKLVIPHEANRDAKCLSTIHGKIQE 1813  
hCLASP2 ---VHFNE DVLME LLEQCADGLWKAERYELIADIYKLIPIYEKRR----- 1677  
hCLASP7 CSGKHFTELGLVGLLEQAAGYFTMGGLYEAVNEVYKNLIPILEAHRDYKKLA AVHGKIQE 1732  
hCLASP1 ---TPYNE NILVEQLYMCGEFLWKSEYELIADVNKPIIAVF EKQDFKKLSDIYYDIHR 1852  
: . \* : : \* : : : : \* : : : : \* : . \*

ITAM DOCK motif DOCK motif ITAM  
hCLASP4 AFTKILEVMHTKKRLGLTFFRVAFYQGQSFEEEDGKEYIYKEPKLTGLSEISLRVLYG 1739  
hCLASP5 AFDSIYNKDH--KRMFGTYFRVGFYFG-SKFGDLDEQEFYKEPAITKLPEISHRLEAFY 1750  
hCLASP3 AFSKIYHQSTGWERMFGTYFRVGFYFG-TKFGDLDEQEFYKEPAITKLAEISHRLEGFY 1872  
hCLASP2 -----DFFEDE DGKEYIYKEPKLTPLSEISQRLLKIYS 1710  
hCLASP7 AFTKIMHQSSGWERVFGTYFRVGFYFG-AHFGDLDEQEFYKEPSITKLAEISHRLEEFYT 1791  
hCLASP1 SYLKVAEVVNSEKRLFGRIYRVAFYQGQSFEEEDGKEYIYKEPKLTGLSEISQRLLKIYA 1912  
\* : : : \* : : \* : : \* : : \*

FIG. 7 (5 of 6)

	ITAM	ITAM	
hCLASP4	EKEFGTENVKIIQDS	DKPVNAKELDPKYAH	IQVITYVKHYFDDKELTERKTEFERNNHNSR
hCLASP5	QCFCGAEFVEVIK	DSTPVDKTKLDPN	KAYIQITTFVEHYFDEYEMKDRVITYFEKNFNLRRFM
hCLASP3	ERFEGEDVVEVIK	DSNPVDCKLDPN	KAYIQITTYVEHYFDTYEMKDRITYFDKNYNLRRFM
hCLASP2	DKFGSENVKMIQ	DSGKVNPKDLDS	KAYIQVTHVHIFHFFDEKELQERKTEFERSHNIRRFM
hCLASP7	ERFEGDDVVEIK	DSYPVDKSKLDS	QKAYIQITTYVEHYFDTYELKDRVITYFDNRNYGLRTFL
hCLASP1	DKFEGADNVKIIQ	DSNVKNPKDLDP	KYAYIQVITYVTHFFEEKEIEDRKTDFEMHHNNINRFV
	: ** : * : : * : * *	: . * : : * : * :	: * : : * * : * : : * :
		ITAM	DOCK motif
hCLASP4	FEAPYTLSGKKQGC	IEEQCKRRTILTST	NSFFYVKKRIPINCEQQINLKPIDGATDEIKD
hCLASP5	YTTPFTLEGRPRG	ELHEQYRRNTVLTM	HAFYIKTRISVIOKEEFVLTPIEVAIEDMCK
hCLASP3	YCTPFTLDGRAH	GELHEQFKRKTILT	SHAFYIKTRVNVTHKEEIIILTPIEVAIEDMQK
hCLASP2	FEMPFTQTGKRQ	GGVEEQCKRRTILT	AIHCFYVKKRIPVMYQHHTDLNPIEVAIDEMSK
hCLASP7	FCTPFTPDGRAH	GELPEQHKKRKTLL	SDHAFYIKTRIRVCHREETVLTPIEVAIEDMQK
hCLASP1	FCTPFTLSGKKH	GGVEEQCKRRTILT	SHLFFYVKKRIQVISQSTELNPIEVAIDEMSR
	: * : * * : * : * : * : * : * : *	: * : * : * : * : *	: * : * : * : * : *
	Coiled-coil		
hCLASP4	KTAEQLKLCSSST	DVMDIQLQLKLQ	GVWSVQVNAGPLAYARAFNLDSQASKYPKKVSELK
hCLASP5	KTLQLAVAINQEP	PDAKMLQMVLCQ	SVGATVNQGPLEVAQVFLAEIPADPKLYRHHNKLK
hCLASP3	KTQELAFATHQDP	ADPKMLQMVLCQ	SVGTTVNQGPLEVAQVFLSEIPSDPKLFRHHNKLK
hCLASP2	KVAELRQLCSSAE	VDMIKLQLKLQ	GSVSVQVNAGPLAYARAFLLDNTNKRYPDNKVKLLK
hCLASP7	KTRELAFATEQDP	PDAKMLQMVLCQ	SVGPTVNQGPLEVAQVFLAEIPEDPKLFRHHNKLK
hCLASP1	KVSELNQLCTME	EVDMISLQLKLQ	GSVSVKVNAGPMAYARAFLEETNAKKYPDNQVKLLK
	* : *	* * : * * *	* : * * : * : * : * : * : *
	Coiled-coil		
hCLASP4	DMFRKFIQACSI	ALELNERLIKEDQ	VEYHEGLKSNFRDMVKELSDITHEQILQEDTMHSP
hCLASP5	LCFKEFIMRCGE	AVEKNKRLITADQ	REYQQLKKNYNKLKENLRPMIERKIPELYKPIFR
hCLASP3	LCFKDFTEKCED	ALRNKNSLIGPVQ	KEYQRELKGLSSP-----
hCLASP2	EVFRQDVEACG	ALAVNERLIKEDQ	LEYQEEMKANYREMAKELSEIMHEQICPLEEKTS-
hCLASP7	LCFKDFCKKCED	ALRNKALIGPDQ	KEYHRELERNYCRLREALQPLLTLQRLPQLMAPTP-
hCLASP1	EIFRQFADACG	ALDVNERLIKEDQ	LEYQEELRSHYKMDLSELSTVMNEQITGRDDLSKR
	* : *	* : * : * * *	* * : * : *
	PDZ ligand		
hCLASP4	WMSNTLHVFC	AISGTSSDRGYGSP	RAEV- 2008
hCLASP5	VESQKRDSF	HRSSFRKCETQLS	QSGS----- 2015
hCLASP3	-----		
hCLASP2	VLPNSLHIF	NAISGTPPTSTMV	HGMTSSSSVM 1980
hCLASP7	--PGLRNSL	NRASFRKADL-----	
hCLASP1	GVDQTCTRV	ISKATPALPTVS	ISSRAEV- 2180